SEQUENCE LISTING

<110> Pagano, M.

<120> METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS

<130> 5914-090-999

<140> To be assigned
<141> 2002-01-07

<150> 60/260,179
<151> 2001-01-5

<160> 89

<170> PatentIn Ver. 2.0

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<213> Homo sapiens

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Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu Lys
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Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp
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Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln
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His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe
    130                 135                 140

Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile
145                 150                 155                 160

Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys
                165                 170                 175

Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu
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Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu
        195                 200                 205

Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp Gly
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Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg His Ser
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Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr Cys
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Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn Thr
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Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe Asp Asn
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Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val Trp Asp
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Ser Arg Thr Tyr Thr Tyr Ile Ser Arg
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Glu Thr Leu Leu Lys Arg Asp Phe Leu Lys Leu Leu Pro Leu Glu Leu
50 55 60

Ser Phe Tyr Leu Leu Lys Trp Leu Asp Pro Gln Thr Leu Leu Thr Cys
65 70 75 80

Cys Leu Val Ser Lys Gln Trp Asn Lys Val Ile Ser Ala Cys Thr Glu
85 90 95

Val Trp Gln Thr Ala Cys Lys Asn Leu Gly Trp Gln Ile Asp Asp Ser
100 105 110

Val Gln Asp Ala Leu His Trp Lys Lys Val Tyr Leu Lys Ala Ile Leu
115 120 125

Arg Met Lys Gln Leu Glu Asp His Glu Ala Phe Glu Thr Ser Ser Leu
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Ile Gly His Ser Ala Arg Val Tyr Ala Leu Tyr Tyr Lys Asp Gly Leu
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Leu Cys Thr Gly Ser Asp Asp Leu Ser Ala Lys Leu Trp Asp Val Ser
165 170 175

Thr Gly Gln Cys Val Tyr Gly Ile Gln Thr His Thr Cys Ala Ala Val
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Lys Phe Asp Glu Gln Lys Leu Val Thr Gly Ser Phe Asp Asn Thr Val
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Ala Cys Trp Glu Trp Ser Ser Gly Ala Arg Thr Gln His Phe Arg Gly
    210                 215                 220

His Thr Gly Ala Val Phe Ser Val Asp Tyr Asn Asp Glu Leu Asp Ile
225                 230                 235                 240

Leu Val Ser Gly Ser Ala Asp Phe Thr Val Lys Val Trp Ala Leu Ser
                245                 250                 255

Ala Gly Thr Cys Leu Asn Thr Leu Thr Gly His Thr Glu Trp Val Thr
            260                 265                 270

Lys Val Val Leu Gln Lys Cys Lys Val Lys Ser Leu Leu His Ser Pro
        275                 280                 285

Gly Asp Tyr Ile Leu Leu Ser Ala Asp Lys Tyr Glu Ile Lys Ile Trp
    290                 295                 300

Pro Ile Gly Arg Glu Ile Asn Cys Lys Cys Leu Lys Thr Leu Ser Val
305                 310                 315                 320

Ser Glu Asp Arg Ser Ile Cys Leu Gln Pro Arg Leu His Phe Asp Gly
                325                 330                 335

Lys Tyr Ile Val Cys Ser Ser Ala Leu Gly Leu Tyr Gln Trp Asp Phe
            340                 345                 350

Ala Ser Tyr Asp Ile Leu Arg Val Ile Lys Thr Pro Glu Ile Ala Asn
        355                 360                 365

Leu Ala Leu Leu Gly Phe Gly Asp Ile Phe Ala Leu Leu Phe Asp Asn
    370                 375                 380

Arg Tyr Leu Tyr Ile Met Asp Leu Arg Thr Glu Ser Leu Ile Ser Arg
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Trp Pro Leu Pro Glu Tyr Arg Glu Ser Lys Arg Gly Ser Ser Phe Leu
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Thr Cys Asp Trp Gly Asn Leu Leu Gln Asp Ile Ile Leu Gln Val Phe
35 40 45

Lys Tyr Leu Pro Leu Leu Asp Arg Ala His Ala Ser Gln Val Cys Arg
50 55 60

Asn Trp Asn Gln Val Phe His Met Pro Asp Leu Trp Arg Cys Phe Glu
65 70 75 80

Phe Glu Leu Asn Gln Pro Ala Thr Ser Tyr Leu Lys Ala Thr His Pro
85 90 95

Glu Leu Ile Lys Gln Ile Ile Lys Arg His Ser Asn His Leu Gln Tyr
100 105 110

Val Ser Phe Lys Val Asp Ser Ser Lys Glu Ser Ala Glu Ala Ala Cys
115 120 125

Asp Ile Leu Ser Gln Leu Val Asn Cys Ser Leu Lys Thr Leu Gly Leu
130 135 140

Ile Ser Thr Ala Arg Pro Ser Phe Met Asp Leu Pro Lys Ser His Phe
145 150 155 160

Ile Ser Ala Leu Thr Val Val Phe Val Asn Ser Lys Ser Leu Ser Ser
165 170 175

Leu Lys Ile Asp Asp Thr Pro Val Asp Asp Pro Ser Leu Lys Val Leu
180 185 190

Val Ala Asn Asn Ser Asp Thr Leu Lys Leu Leu Lys Met Ser Ser Cys
195 200 205

Pro His Val Ser Pro Ala Gly Ile Leu Cys Val Ala Asp Gln Cys His
210 215 220

Gly Leu Arg Glu Leu Ala Leu Asn Tyr His Leu Leu Ser Asp Glu Leu

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Leu Leu Ala Leu Ser Ser Glu Lys His Val Arg Leu Glu His Leu Arg
                245                 250                 255

Ile Asp Val Val Ser Glu Asn Pro Gly Gln Thr His Phe His Thr Ile
            260                 265                 270

Gln Lys Ser Ser Trp Asp Ala Phe Ile Arg His Ser Pro Lys Val Asn
        275                 280                 285

Leu Val Met Tyr Phe Phe Leu Tyr Glu Glu Glu Phe Asp Pro Phe Phe
    290                 295                 300

Arg Tyr Glu Ile Pro Ala Thr His Leu Tyr Phe Gly Arg Ser Val Ser
305                 310                 315                 320

Lys Asp Val Leu Gly Arg Val Gly Met Thr Cys Pro Arg Leu Val Glu
                325                 330                 335

Leu Val Val Cys Ala Asn Gly Leu Arg Pro Leu Asp Glu Glu Leu Ile
            340                 345                 350

Arg Ile Ala Glu Arg Cys Lys Asn Leu Ser Ala Ile Gly Leu Gly Glu
        355                 360                 365

Cys Glu Val Ser Cys Ser Ala Phe Val Glu Phe Val Lys Met Cys Gly
    370                 375                 380

Gly Arg Leu Ser Gln Leu Ser Ile Met Glu Glu Val Leu Ile Pro Asp
385                 390                 395                 400

Gln Lys Tyr Ser Leu Glu Gln Ile His Trp Glu Val Ser Lys His Leu
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         35                  40                  45

Arg Glu Glu Val Asp Glu Ala Ala Ser Thr Leu Thr Arg Leu Pro Ile
     50                  55                  60

Asp Val Gln Leu Tyr Ile Leu Ser Phe Leu Ser Pro His Asp Leu Cys
 65                  70                  75                  80

Gln Leu Gly Ser Thr Asn His Tyr Trp Asn Glu Thr Val Arg Asn Pro
                 85                  90                  95

Ile Leu Trp Arg Tyr Phe Leu Leu Arg Asp Leu Pro Ser Trp Ser Ser
            100                 105                 110

Val Asp Trp Lys Ser Leu Pro Tyr Leu Gln Ile Leu Lys Lys Pro Ile
        115                 120                 125

Ser Glu Val Ser Asp Gly Ala Phe Phe Asp Tyr Met Ala Val Tyr Leu
    130                 135                 140

Met Cys Cys Pro Tyr Thr Arg Arg Ala Ser Lys Ser Ser Arg Pro Met
145                 150                 155                 160

Tyr Gly Ala Val Thr Ser Phe Leu His Ser Leu Ile Ile Pro Asn Glu
                165                 170                 175

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            180                 185                 190

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    210                 215                 220

Leu Asn Asn Gln His Lys Phe Asn Ile Leu Ile Leu Tyr Ser Thr Thr
225                 230                 235                 240

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Lys Met Phe Ser Arg His Asn Glu Gly Asp Asp Arg Pro Gly Ser Arg
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Lys Arg Met Pro Cys Phe Tyr Leu Ala His Glu Leu His Leu Asn Leu
            340                 345                 350

Leu Asn His Pro Trp Leu Val Gln Asp Thr Glu Ala Glu Thr Leu Thr
        355                 360                 365

Gly Phe Leu Asn Gly Ile Glu Trp Ile Leu Glu Glu Val Glu Ser Lys
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Arg Ala Arg Phe Ser Phe Gln Ile Leu Gly Thr Glu Thr Ile Asn Leu
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Leu Leu Arg Ser Cys Glu Tyr Leu Leu Ser Gln Pro Thr Leu Ser Cys
                405                 410                 415

Leu Phe Ala Asp Arg Leu Ser Phe Gly Gln Leu Leu Leu Cys Phe Leu
            420                 425                 430

Tyr Tyr Phe Tyr Phe Leu Pro Ile Asn Tyr Lys Lys Arg Val Ser Val
        435                 440                 445

Leu Val Phe Ser Pro Lys Met Asn Leu Thr Phe Phe Trp Phe Leu Tyr
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465                 470
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<210> 10
<211> 447
<212> PRT
<213> Homo sapiens

<400> 10
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Cys Ser Ala Ser Pro Ser Ala Val Thr Ala Ala Gly Arg Pro Arg Pro
20 25 30

Ser Asp Ser Cys Lys Glu Glu Ser Ser Thr Leu Ser Val Lys Met Lys
35 40 45

Cys Asp Phe Asn Cys Asn His Val His Ser Gly Leu Lys Leu Val Lys
50 55 60

Pro Asp Asp Ile Gly Arg Leu Val Ser Tyr Thr Pro Ala Tyr Leu Glu
65 70 75 80

Gly Ser Cys Lys Asp Cys Ile Lys Asp Tyr Glu Arg Leu Ser Cys Ile
85 90 95

Gly Ser Pro Ile Val Ser Pro Arg Ile Val Gln Leu Glu Thr Glu Ser
100 105 110

Lys Arg Leu His Asn Lys Glu Asn Gln His Val Gln Gln Thr Leu Asn
115 120 125

Ser Thr Asn Glu Ile Glu Ala Leu Glu Thr Ser Arg Leu Tyr Glu Asp
130 135 140

Ser Gly Tyr Ser Ser Phe Ser Leu Gln Ser Gly Leu Ser Glu His Glu
145 150 155 160

Glu Gly Ser Leu Leu Glu Glu Asn Phe Gly Asp Ser Leu Gln Ser Cys
165 170 175

Leu Leu Gln Ile Gln Ser Pro Asp Gln Tyr Pro Asn Lys Asn Leu Leu
180 185 190

```
Pro Val Leu His Phe Glu Lys Val Val Cys Ser Thr Leu Lys Lys Asn
        195                 200                 205

Ala Lys Arg Asn Pro Lys Val Asp Arg Glu Met Leu Lys Glu Ile Ile
    210                 215                 220

Ala Arg Gly Asn Phe Arg Leu Gln Asn Ile Ile Gly Arg Lys Met Gly
225                 230                 235                 240

Leu Glu Cys Val Asp Ile Leu Ser Glu Leu Phe Arg Arg Gly Leu Arg
                245                 250                 255

His Val Leu Ala Thr Ile Leu Ala Gln Leu Ser Asp Met Asp Leu Ile
            260                 265                 270

Asn Val Ser Lys Val Ser Thr Thr Trp Lys Lys Ile Leu Glu Asp Asp
        275                 280                 285

Lys Gly Ala Phe Gln Leu Tyr Ser Lys Ala Ile Gln Arg Val Thr Glu
    290                 295                 300

Asn Asn Asn Lys Phe Ser Pro His Ala Ser Thr Arg Glu Tyr Val Met
305                 310                 315                 320

Phe Arg Thr Pro Leu Ala Ser Val Gln Lys Ser Ala Ala Gln Thr Ser
                325                 330                 335

Leu Lys Lys Asp Ala Gln Thr Lys Leu Ser Asn Gln Gly Asp Gln Lys
            340                 345                 350

Gly Ser Thr Tyr Ser Arg His Asn Glu Phe Ser Glu Val Ala Lys Thr
        355                 360                 365

Leu Lys Lys Asn Glu Ser Leu Lys Ala Cys Ile Arg Cys Asn Ser Pro
    370                 375                 380

Ala Lys Tyr Asp Cys Tyr Leu Gln Arg Ala Thr Cys Lys Arg Glu Gly
385                 390                 395                 400

Cys Gly Phe Asp Tyr Cys Thr Lys Cys Leu Cys Asn Tyr His Thr Thr
                405                 410                 415

Lys Asp Cys Ser Asp Gly Lys Leu Leu Lys Ala Ser Cys Lys Ile Gly
            420                 425                 430

Pro Leu Pro Gly Thr Lys Lys Ser Lys Lys Asn Leu Arg Arg Leu
        435                 440                 445
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<210> 11
<211> 1535
<212> DNA
<213> Homo sapiens

<400> 11
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aataaatggt tttcagtaaa aaaaaaaaaa aaaaa 1535

<210> 12
<211> 338
<212> PRT
<213> Homo sapiens

<400> 12
Ala Arg Ser Gly Ala Ser Ala Leu Arg Arg Arg Arg Val Gln Val Trp
1 5 10 15

Val Leu Ser Arg Pro Pro Pro Gly Gly Gly Asp Ser Phe Arg Thr Arg
20 25 30

Arg Pro Gln Arg Gly Pro Gly Pro Gly Gly Ser Gln Ala Met Asp Ala
35 40 45

Pro His Ser Lys Ala Ala Leu Asp Ser Ile Asn Glu Leu Pro Asp Asn
50 55 60

Ile Leu Leu Glu Leu Phe Thr His Val Pro Ala Arg Gln Leu Leu Leu
65 70 75 80

Asn Cys Arg Leu Val Cys Ser Leu Trp Arg Asp Leu Ile Asp Leu Leu
85 90 95

Thr Leu Trp Lys Arg Lys Cys Leu Arg Lys Gly Phe Ile Thr Lys Asp
100 105 110

Trp Asp Gln Pro Val Ala Asp Trp Lys Ile Phe Tyr Phe Leu Arg Ser
115 120 125

Leu His Arg Asn Leu Leu Arg Asn Pro Cys Ala Glu Asn Asp Met Phe
130 135 140

Ala Trp Gln Ile Asp Phe Asn Gly Gly Asp Arg Trp Lys Val Asp Ser
145 150 155 160

Leu Pro Gly Ala His Gly Thr Glu Phe Pro Asp Pro Lys Val Lys Lys
165 170 175

Ser Phe Val Thr Ser Tyr Glu Leu Cys Leu Lys Trp Glu Leu Val Asp
180 185 190

Leu Leu Ala Asp Arg Tyr Trp Glu Glu Leu Leu Asp Thr Phe Arg Pro
195 200 205

Asp Ile Val Val Lys Asp Trp Phe Ala Ala Arg Ala Asp Cys Gly Cys
    210   215   220

Thr Tyr Gln Leu Lys Val Gln Leu Ala Ser Ala Asp Tyr Phe Val Leu
225   230   235   240

Ala Ser Phe Glu Pro Pro Pro Val Thr Ile Gln Gln Trp Asn Asn Ala
                245   250   255

Thr Trp Thr Glu Val Ser Tyr Thr Phe Ser Asp Tyr Pro Arg Gly Val
            260   265   270

Arg Tyr Ile Leu Phe Gln His Gly Gly Arg Asp Thr Gln Tyr Trp Ala
        275   280   285

Gly Trp Tyr Gly Pro Arg Val Thr Asn Ser Ser Ile Val Val Ser Pro
    290   295   300

Lys Met Thr Arg Asn Gln Ala Ser Ser Glu Ala Gln Pro Gly Gln Lys
305   310   315   320

His Gly Gln Glu Glu Ala Ala Gln Ser Pro Tyr Gly Ala Val Val Gln
                325   330   335

Ile Phe

<210> 13
<211> 1763
<212> DNA
<213> Homo sapiens

<400> 13
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gtttgattct tcacgatgac attccaccgc ctaatatacc ttcatccaca gattcagagc 180
attcttcact ccagaacaat gagcaaccct ctttggccac cagctccaat cagactagca 240
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atgacgacag tatgttaggg cctagtcaaa attttgaagc tgagtcaatt caagataatg 360
cgcatatggc agagggcaca ggtttctatc cctcagaacc cctgctctgt agtgaatcgg 420
tggaagggca agtgccacat tcattagaga ccttgtatca atcagctgac tgttctgatg 480
ccaatgatgc gttgatagtg ttgatacatc ttctcatgtt ggagtcaggt tacatacctc 540
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agctgcagta catgcatcat ctctgcgagg gcagctccgc tactctcacc tgtgtgcctt 660
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aaagattgca gctgctacca gaatctttta tttgcaaaga gaaactaggg gaaaatgtag 780
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tacctccact gagaccacgc tttgatccag ttggcccact tccaggacct aaccccatct 1380
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gattgtggtg ttgagagttg cactcccaga aaccttttaa gagatacatt tatagcccta 1620
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cagattaaaa aaaagtgtaa att 1763

<210> 14
<211> 482
<212> PRT
<213> Homo sapiens

<400> 14

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Met Ser Asn Thr Arg Phe Thr Ile Thr Leu Asn Tyr Lys Asp Pro Leu
  1               5                  10                  15

Thr Gly Asp Glu Glu Thr Leu Ala Ser Tyr Gly Ile Val Ser Gly Asp
             20                  25                  30

Leu Ile Cys Leu Ile Leu His Asp Asp Ile Pro Pro Pro Asn Ile Pro
         35                  40                  45

Ser Ser Thr Asp Ser Glu His Ser Ser Leu Gln Asn Asn Glu Gln Pro
     50                  55                  60

Ser Leu Ala Thr Ser Ser Asn Gln Thr Ser Ile Gln Asp Glu Gln Pro
 65                  70                  75                  80

Ser Asp Ser Phe Gln Gly Gln Ala Ala Gln Ser Gly Val Trp Asn Asp
                 85                  90                  95

Asp Ser Met Leu Gly Pro Ser Gln Asn Phe Glu Ala Glu Ser Ile Gln
            100                 105                 110

Asp Asn Ala His Met Ala Glu Gly Thr Gly Phe Tyr Pro Ser Glu Pro
        115                 120                 125

Leu Leu Cys Ser Glu Ser Val Glu Gly Gln Val Pro His Ser Leu Glu
    130                 135                 140

Thr Leu Tyr Gln Ser Ala Asp Cys Ser Asp Ala Asn Asp Ala Leu Ile
145                 150                 155                 160

Val Leu Ile His Leu Leu Met Leu Glu Ser Gly Tyr Ile Pro Gln Gly
                165                 170                 175

Thr Glu Ala Lys Ala Leu Ser Leu Pro Glu Lys Trp Lys Leu Ser Gly
            180                 185                 190

Val Tyr Lys Leu Gln Tyr Met His His Leu Cys Glu Gly Ser Ser Ala
        195                 200                 205

Thr Leu Thr Cys Val Pro Leu Gly Asn Leu Ile Val Val Asn Ala Thr
    210                 215                 220

Leu Lys Ile Asn Asn Glu Ile Arg Ser Val Lys Arg Leu Gln Leu Leu
225                 230                 235                 240

Pro Glu Ser Phe Ile Cys Lys Glu Lys Leu Gly Glu Asn Val Ala Asn
                245                 250                 255

Ile Tyr Lys Asp Leu Gln Lys Leu Ser Arg Leu Phe Lys Asp Gln Leu
            260                 265                 270

Val Tyr Pro Leu Leu Ala Phe Thr Arg Gln Ala Leu Asn Leu Pro Asn
        275                 280                 285

Val Phe Gly Leu Val Val Leu Pro Leu Glu Leu Lys Leu Arg Ile Phe
```

```
    290                 295                 300

Arg Leu Leu Asp Val Arg Ser Val Leu Ser Leu Ser Ala Val Cys Arg
305                 310                 315                 320

Asp Leu Phe Thr Ala Ser Asn Asp Pro Leu Leu Trp Arg Phe Leu Tyr
                325                 330                 335

Leu Arg Asp Phe Arg Asp Asn Thr Val Arg Val Gln Asp Thr Asp Trp
            340                 345                 350

Lys Glu Leu Tyr Arg Lys Arg His Ile Gln Arg Lys Glu Ser Pro Lys
        355                 360                 365

Gly Arg Phe Val Leu Leu Leu Pro Ser Ser Thr His Thr Ile Pro Phe
    370                 375                 380

Tyr Pro Asn Pro Leu His Pro Arg Pro Phe Pro Ser Ser Arg Leu Pro
385                 390                 395                 400

Pro Gly Ile Ile Gly Gly Glu Tyr Asp Gln Arg Pro Thr Leu Pro Tyr
                405                 410                 415

Val Gly Asp Pro Ile Ser Ser Leu Ile Pro Gly Pro Gly Glu Thr Pro
            420                 425                 430

Ser Gln Leu Pro Pro Leu Arg Pro Arg Phe Asp Pro Val Gly Pro Leu
        435                 440                 445

Pro Gly Pro Asn Pro Ile Leu Pro Gly Arg Gly Gly Pro Asn Asp Arg
    450                 455                 460

Phe Pro Phe Arg Pro Ser Arg Gly Arg Pro Thr Asp Gly Arg Leu Ser
465                 470                 475                 480

Phe Met
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<210> 15
<211> 43
<212> PRT
<213> Homo sapiens

<400> 15
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Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile Leu Ser Tyr
  1               5                  10                  15

Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys Lys Glu Trp
            20                  25                  30

Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys
        35                  40
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<210> 16
<211> 40
<212> PRT
<213> Homo sapiens

<400> 16
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Leu Pro Leu Glu Leu Ser Phe Tyr Leu Leu Lys Trp Leu Asp Pro Gln
  1               5                  10                  15
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Thr Leu Leu Thr Cys Cys Leu Val Ser Lys Gln Trp Asn Lys Val Ile
20 25 30

Ser Ala Cys Thr Glu Val Trp Gln
35 40

<210> 17
<211> 39
<212> PRT
<213> Homo sapiens

<400> 17
Leu Leu Gln Asp Ile Ile Leu Gln Val Phe Lys Tyr Leu Pro Leu Leu
1 5 10 15

Asp Arg Ala His Ala Ser Gln Val Cys Arg Asn Trp Asn Gln Val Phe
20 25 30

His Met Pro Asp Leu Trp Arg
35

<210> 18
<211> 39
<212> PRT
<213> Homo sapiens

<400> 18
Leu Pro Ile Asp Val Gln Leu Tyr Ile Leu Ser Phe Leu Ser Pro His
1 5 10 15

Asp Leu Cys Gln Leu Gly Ser Thr Asn His Tyr Trp Asn Glu Thr Val
20 25 30

Arg Asn Pro Ile Leu Trp Arg
35

<210> 19
<211> 39
<212> PRT
<213> Homo sapiens

<400> 19
Leu Arg His Val Leu Ala Thr Ile Leu Ala Gln Leu Ser Asp Met Asp
1 5 10 15

Leu Ile Asn Val Ser Lys Val Ser Thr Thr Trp Lys Lys Ile Leu Glu
20 25 30

Asp Asp Lys Gly Ala Phe Gln
35

<210> 20
<211> 40
<212> PRT
<213> Homo sapiens

<400> 20
Leu Pro Asp Asn Ile Leu Leu Glu Leu Phe Thr His Val Pro Ala Arg
1 5 10 15

Gln Leu Leu Leu Asn Cys Arg Leu Val Cys Ser Leu Trp Arg Asp Leu
20 25 30

Ile Asp Leu Leu Thr Leu Trp Lys
35 40

<210> 21
<211> 39
<212> PRT
<213> Homo sapiens

<400> 21
Leu Pro Leu Glu Leu Lys Leu Arg Ile Phe Arg Leu Leu Asp Val Arg
1 5 10 15

Ser Val Leu Ser Leu Ser Ala Val Cys Arg Asp Leu Phe Thr Ala Ser
20 25 30

Asn Asp Pro Leu Leu Trp Arg
35

<210> 22
<211> 39
<212> PRT
<213> Homo sapiens

<400> 22
Leu Pro Asp Glu Leu Leu Leu Gly Ile Phe Ser Cys Leu Cys Leu Pro
1 5 10 15

Glu Leu Leu Lys Val Ser Gly Val Cys Lys Arg Trp Tyr Arg Leu Ala
20 25 30

Ser Asp Glu Ser Leu Trp Gln
35

<210> 23
<211> 1323
<212> DNA
<213> Homo sapiens

<400> 23
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catacacaca cggttcttct agactggggg agtttgcctc accatgtagt attacaaatt 180
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<210> 24
<211> 434
<212> PRT
<213> Homo sapiens

<400> 24

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Met Lys Arg Asn Ser Leu Ser Val Glu Asn Lys Ile Val Gln Leu Ser
  1               5                  10                  15

Gly Ala Ala Lys Gln Pro Lys Val Gly Phe Tyr Ser Ser Leu Asn Gln
             20                  25                  30

Thr His Thr His Thr Val Leu Leu Asp Trp Gly Ser Leu Pro His His
         35                  40                  45

Val Val Leu Gln Ile Phe Gln Tyr Leu Pro Leu Leu Asp Arg Ala Cys
     50                  55                  60

Ala Ser Ser Val Cys Arg Arg Trp Asn Glu Val Phe His Ile Ser Asp
 65                  70                  75                  80

Leu Trp Arg Lys Phe Glu Phe Glu Leu Asn Gln Ser Ala Thr Ser Ser
                 85                  90                  95

Phe Lys Ser Thr His Pro Asp Leu Ile Gln Gln Ile Ile Lys Lys His
            100                 105                 110

Phe Ala His Leu Gln Tyr Val Ser Phe Lys Val Asp Ser Ser Ala Glu
        115                 120                 125

Ser Ala Glu Ala Ala Cys Asp Ile Leu Ser Gln Leu Val Asn Cys Ser
    130                 135                 140

Ile Gln Thr Leu Gly Leu Ile Ser Thr Ala Lys Pro Ser Phe Met Asn
145                 150                 155                 160

Val Ser Glu Ser His Phe Val Ser Ala Leu Thr Val Val Phe Ile Asn
                165                 170                 175

Ser Lys Ser Leu Ser Ser Ile Lys Ile Glu Asp Thr Pro Val Asp Asp
            180                 185                 190

Pro Ser Leu Lys Ile Leu Val Ala Asn Asn Ser Asp Thr Leu Arg Leu
        195                 200                 205

Pro Lys Met Ser Ser Cys Pro His Val Ser Ser Asp Gly Ile Leu Cys
    210                 215                 220

Val Ala Asp Arg Cys Gln Gly Leu Arg Glu Leu Ala Leu Asn Tyr Tyr
225                 230                 235                 240

Ile Leu Thr Asp Glu Leu Phe Leu Ala Leu Ser Ser Glu Thr His Val
                245                 250                 255

Asn Leu Glu His Leu Arg Ile Asp Val Val Ser Glu Asn Pro Gly Gln
            260                 265                 270
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Ile Lys Phe His Ala Val Lys Lys His Ser Trp Asp Ala Leu Ile Lys
        275                 280                 285

His Ser Pro Arg Val Asn Val Val Met His Phe Phe Leu Tyr Glu Glu
    290                 295                 300

Glu Phe Glu Thr Phe Phe Lys Glu Glu Thr Pro Val Thr His Leu Tyr
305                 310                 315                 320

Phe Gly Arg Ser Val Ser Lys Val Val Leu Gly Arg Val Gly Leu Asn
                325                 330                 335

Cys Pro Arg Leu Ile Glu Leu Val Val Cys Ala Asn Asp Leu Gln Pro
            340                 345                 350

Leu Asp Asn Glu Leu Ile Cys Ile Ala Glu His Cys Thr Asn Leu Thr
        355                 360                 365

Ala Leu Gly Leu Ser Lys Cys Glu Val Ser Cys Ser Ala Phe Ile Arg
    370                 375                 380

Phe Val Arg Leu Cys Glu Arg Arg Leu Thr Gln Leu Ser Val Met Glu
385                 390                 395                 400

Glu Val Leu Ile Pro Asp Glu Asp Tyr Ser Leu Asp Glu Ile His Thr
                405                 410                 415

Glu Val Ser Lys Tyr Leu Gly Arg Val Trp Phe Pro Asp Val Met Pro
            420                 425                 430

Leu Trp
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<210> 25
<211> 1970
<212> DNA
<213> Homo sapiens

<400> 25
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gcaacaagaa ggctacagtg agcaaggcta cctcaccaga gagcagagca ggagaatggc 360
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tcatcttttg aaggcaagga aatcgaaaga acaggaagga ttcattaatt tggaaatgtt 480
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gcaaaactgg cagttatttt tataatataa atttataatt tgatttttta ttttaaaaac 1860
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ttatgattta cattcatagg aataaaataa aatatyatta gaactctggt 1970

<210> 26
<211> 634
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> all Xaa positions
<223> Xaa=unknown amino acid residue

<400> 26
Glu Thr Ser Lys Leu Gly Ser Ala Val Leu Ala Pro Ala Ala Gly Gly
1 5 10 15

Thr Leu Ser Ser Glu Gly Arg Ser Ala Val Ser Gly Ile Leu Ile Ala
20 25 30

Val Thr Ser Thr Gly Val Asp Lys Ser Leu Asn Gln Leu Leu His Gly
35 40 45

Leu Gly Thr Ser Ser Arg Leu Ser His Phe Pro Phe Gly Lys Ser Pro
50 55 60

Pro Arg Gly Gln Phe Val Ala Ala Ala Val Glu Ile Ala Gly Arg Ser
65 70 75 80

Gly Leu Gln Met Gly Gln Gly Leu Trp Arg Val Val Arg Asn Gln Gln
85 90 95

Leu Gln Gln Glu Gly Tyr Ser Glu Gln Gly Tyr Leu Thr Arg Glu Gln
100 105 110

Ser Arg Arg Met Ala Ala Ser Asn Ile Ser Asn Thr Asn His Arg Lys
115 120 125

Gln Val Gln Gly Gly Ile Asp Ile Tyr His Leu Leu Lys Ala Arg Lys
130 135 140

Ser Lys Glu Gln Glu Gly Phe Ile Asn Leu Glu Met Leu Pro Pro Glu
145 150 155 160

Leu Ser Phe Thr Ile Leu Ser Tyr Leu Asn Ala Thr Asp Leu Cys Leu
165 170 175

Ala Ser Cys Val Trp Gln Asp Leu Ala Asn Asp Glu Leu Leu Trp Gln
180 185 190

Gly Leu Cys Lys Ser Thr Trp Gly His Cys Ser Ile Tyr Asn Lys Asn
195 200 205

Pro Pro Leu Gly Phe Ser Phe Arg Lys Xaa Tyr Met Gln Leu Asp Glu
210 215 220

Gly Ser Leu Thr Phe Asn Ala Asn Pro Asp Glu Gly Val Asn Tyr Phe
225 230 235 240

Met Ser Lys Gly Ile Leu Asp Asp Ser Pro Lys Glu Ile Ala Lys Phe
245 250 255

Ile Phe Cys Thr Arg Thr Leu Asn Trp Lys Lys Leu Arg Ile Tyr Leu
260 265 270

Asp Glu Arg Arg Asp Val Leu Asp Asp Leu Val Thr Leu His Asn Phe
275 280 285

Arg Asn Gln Phe Leu Pro Asn Ala Leu Arg Glu Phe Phe Arg His Ile
290 295 300

His Ala Pro Glu Glu Arg Gly Glu Tyr Leu Glu Thr Leu Ile Thr Lys
305 310 315 320

Phe Ser His Arg Phe Cys Ala Cys Asn Pro Asp Leu Met Arg Glu Leu
325 330 335

Gly Leu Ser Pro Asp Ala Val Tyr Val Leu Cys Tyr Ser Leu Ile Leu
340 345 350

Leu Ser Ile Asp Leu Thr Ser Pro His Val Lys Asn Lys Met Ser Lys
355 360 365

Arg Glu Phe Ile Arg Asn Thr Arg Arg Ala Ala Gln Asn Ile Ser Glu
370 375 380

Asp Phe Val Gly His Leu Tyr Asp Asn Ile Tyr Leu Ile Gly His Val
385 390 395 400

Ala Ala Lys Ala Gln Leu Leu Gly Leu Gln Phe Leu Leu Gln Thr Lys
405 410 415

Ala Thr Gln Gly Leu Ser Arg Tyr Gly Gly Tyr Ile Ser Ala Gly His
420 425 430

Cys Ser Leu Ser Ile Gln Ser Ser Phe Ser Val Gln Pro Phe Phe Leu
435 440 445

Leu Pro Phe Ser Ile Leu Val Ile Ser Leu Gly Asn Ile Ile Leu Gln
450 455 460

Asn Phe Ser Phe Cys Leu Ser Arg Phe Ala Gln Ser Arg Ala Thr Val
465 470 475 480

His Ser Cys Arg Met Ile Asn His Tyr Thr Leu Lys Asp Gly Val Phe
485 490 495

Val His Ile Cys Leu Lys Asn Phe Ile His Phe His Ser Leu Tyr Lys
500 505 510

Tyr His Val Met Cys Thr Tyr Leu Thr Lys Glu Ile Tyr Ser His Asn
515 520 525

Tyr Phe Ile Val Lys Ile Leu Thr Lys Val Phe Pro Phe Leu Ser Asn
530 535 540

Val Leu Lys Phe Ile Phe Ser Glu Thr Ile Val Xaa Val Lys Val Arg
545 550 555 560

Ser Asp Phe Arg Gln Lys Pro Ile Pro Ala Ser Phe Ser Phe Lys Leu
565 570 575

Arg Val Leu Ile Cys Tyr Tyr Ile Thr Met Gln Asn Trp Gln Leu Phe
580 585 590

Leu Tyr Lys Phe Ile Ile Phe Phe Ile Leu Lys Thr Gly Leu Ile Lys
595 600 605

Ser Arg Val Leu Thr Ile Asp Phe Asn Ile Lys Ile Tyr Asp Leu His
610 615 620

Ser Glu Asn Lys Ile Xaa Leu Glu Leu Trp
625 630

<210> 27
<211> 4168
<212> DNA
<213> Homo sapiens

<400> 27
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gcggctgcgc gagctgtgcc agagcagcgg gaaggtgtgg aaggagcagt tccgggtgag 240
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taaagttcgg caaaaagctg ggttagaagc gcggaagatt gtagcctcgt tctcaaagag 360
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agagattttt tttgaggatg aactggtgtg tatcctaaat atggaaggaa gaaaagcttt 480
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gaagttagtt gcatattcag aggtaaagtt gtgtgctatc ttggcagcat cttagagatg 2400
gagacattaa caagctaatg gtaattagaa tcatttgaat ttatttttt ctaatatgtg 2460

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<210> 28
<211> 621
<212> PRT
<213> Homo sapiens

<400> 28

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Met Ala Ala Ala Ala Val Asp Ser Ala Met Glu Val Val Pro Ala Leu
  1               5                  10                  15

Ala Glu Glu Ala Ala Pro Glu Val Ala Gly Leu Ser Cys Leu Val Asn
             20                  25                  30

Leu Pro Gly Glu Val Leu Glu Tyr Ile Leu Cys Cys Gly Ser Leu Thr
         35                  40                  45

Ala Ala Asp Ile Gly Arg Val Ser Ser Thr Cys Arg Arg Leu Arg Glu
     50                  55                  60

Leu Cys Gln Ser Ser Gly Lys Val Trp Lys Glu Gln Phe Arg Val Arg
 65                  70                  75                  80

Trp Pro Ser Leu Met Lys His Tyr Ser Pro Thr Asp Tyr Val Asn Trp
                 85                  90                  95

Leu Glu Glu Tyr Lys Val Arg Gln Lys Ala Gly Leu Glu Ala Arg Lys
            100                 105                 110

Ile Val Ala Ser Phe Ser Lys Arg Phe Phe Ser Glu His Val Pro Cys
        115                 120                 125

Asn Gly Phe Ser Asp Ile Glu Asn Leu Glu Gly Pro Glu Ile Phe Phe
    130                 135                 140
```

```
Glu Asp Glu Leu Val Cys Ile Leu Asn Met Glu Gly Arg Lys Ala Leu
145                 150                 155                 160

Thr Trp Lys Tyr Tyr Ala Lys Lys Ile Leu Tyr Tyr Leu Arg Gln Gln
                165                 170                 175

Lys Ile Leu Asn Asn Leu Lys Ala Phe Leu Gln Gln Pro Asp Asp Tyr
            180                 185                 190

Glu Ser Tyr Leu Glu Gly Ala Val Tyr Ile Asp Gln Tyr Cys Asn Pro
        195                 200                 205

Leu Ser Asp Ile Ser Leu Lys Asp Ile Gln Ala Gln Ile Asp Ser Ile
    210                 215                 220

Val Glu Leu Val Cys Lys Thr Leu Arg Gly Ile Asn Ser Arg His Pro
225                 230                 235                 240

Ser Leu Ala Phe Lys Ala Gly Glu Ser Ser Met Ile Met Glu Ile Glu
                245                 250                 255

Leu Gln Ser Gln Val Leu Asp Ala Met Asn Tyr Val Leu Tyr Asp Gln
            260                 265                 270

Leu Lys Phe Lys Gly Asn Arg Met Asp Tyr Tyr Asn Ala Leu Asn Leu
        275                 280                 285

Tyr Met His Gln Val Leu Ile Arg Arg Thr Gly Ile Pro Ile Ser Met
    290                 295                 300

Ser Leu Leu Tyr Leu Thr Ile Ala Arg Gln Leu Gly Val Pro Leu Glu
305                 310                 315                 320

Pro Val Asn Phe Pro Ser His Phe Leu Leu Arg Trp Cys Gln Gly Ala
                325                 330                 335

Glu Gly Ala Thr Leu Asp Ile Phe Asp Tyr Ile Tyr Ile Asp Ala Phe
            340                 345                 350

Gly Lys Gly Lys Gln Leu Thr Val Lys Glu Cys Glu Tyr Leu Ile Gly
        355                 360                 365

Gln His Val Thr Ala Ala Leu Tyr Gly Val Val Asn Val Lys Lys Val
    370                 375                 380

Leu Gln Arg Met Val Gly Asn Leu Leu Ser Leu Gly Lys Arg Glu Gly
385                 390                 395                 400

Ile Asp Gln Ser Tyr Gln Leu Leu Arg Asp Ser Leu Asp Leu Tyr Leu
                405                 410                 415

Ala Met Tyr Pro Asp Gln Val Gln Leu Leu Leu Leu Gln Ala Arg Leu
            420                 425                 430

Tyr Phe His Leu Gly Ile Trp Pro Glu Lys Val Leu Asp Ile Leu Gln
        435                 440                 445

His Ile Gln Thr Leu Asp Pro Gly Gln His Gly Ala Val Gly Tyr Leu
    450                 455                 460

Val Gln His Thr Leu Glu His Ile Glu Arg Lys Lys Glu Glu Val Gly
465                 470                 475                 480
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Val Glu Val Lys Leu Arg Ser Asp Glu Lys His Arg Asp Val Cys Tyr
485 490 495

Ser Ile Gly Leu Ile Met Lys His Lys Arg Tyr Gly Tyr Asn Cys Val
500 505 510

Ile Tyr Gly Trp Asp Pro Thr Cys Met Met Gly His Glu Trp Ile Arg
515 520 525

Asn Met Asn Val His Ser Leu Pro His Gly His His Gln Pro Phe Tyr
530 535 540

Asn Val Leu Val Glu Asp Gly Ser Cys Arg Tyr Ala Ala Gln Glu Asn
545 550 555 560

Leu Glu Tyr Asn Val Glu Pro Gln Glu Ile Ser His Pro Asp Val Gly
565 570 575

Arg Tyr Phe Ser Glu Phe Thr Gly Thr His Tyr Ile Pro Asn Ala Glu
580 585 590

Leu Glu Ile Arg Tyr Pro Glu Asp Leu Glu Phe Val Tyr Glu Thr Val
595 600 605

Gln Asn Ile Tyr Ser Ala Lys Lys Glu Asn Ile Asp Glu
610 615 620

<210> 29
<211> 278
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> all n positions
<223> n=a, c, g or t

<400> 29
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tcccgggntc ctccgtagac ccgcgganac cttcgtgttg agtaacctgg cggaggtggt 120
ggagcgtgtg ctcaccttcc tgcccgccaa ggcgttgctg cgggtggcct gcgtgtgccg 180
cttatggagg gagtgtgtgc gcagagtatt gcggacccat cggagcgtaa cctggatctc 240
cgcaggcctg gcggaggccg gccacctggn ggggcatt 278

<210> 30
<211> 91
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> all Xaa positions
<223> Xaa=unknown amino acid residue

<400> 30
Arg Ser Thr Gly Phe Arg Arg Ala Gly Glu Glu Trp Ser Arg Xaa Leu
1 5 10 15

Ala Ala Ser Pro Gly Xaa Leu Arg Arg Pro Ala Xaa Thr Phe Val Leu
20 25 30

Ser Asn Leu Ala Glu Val Val Glu Arg Val Leu Thr Phe Leu Pro Ala

```
          35                  40                  45

Lys Ala Leu Leu Arg Val Ala Cys Val Cys Arg Leu Trp Arg Glu Cys
      50                  55                  60

Val Arg Arg Val Leu Arg Thr His Arg Ser Val Thr Trp Ile Ser Ala
 65                  70                  75                  80

Gly Leu Ala Glu Ala Gly His Leu Xaa Gly His
                 85                  90
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<210> 31
<211> 592
<212> DNA
<213> Homo sapiens

<400> 31
gcggccgcgc ccggtgcagc aacagcagca gcagcccccg cagcagccgc cgccgcagcc 60
gccccagcag cagccgcccc agcagcagcc tccgccgccg ccgcagcagc agcagcagca 120
gcagcctccg ccgccgccac cgccgcctcc gccgctgcct caggagcgga acaacgtcgg 180
cgagcgggat gatgatgtgc ctgcagatat ggttgcagaa gaatcaggtc ctggtgcaca 240
aaatagtcca taccaacttc gtagaaaaac tcttttgccg aaaagaacag cgtgtcccac 300
aaagaacagt atggagggcg cctcaacttc aactacagaa aactttggtc atcgtgcaaa 360
acgtgcaaga gtgtctggaa aatcacaaga tctatcagca gcacctgctg aacagtatct 420
tcaggagaaa ctgccagatg aagtggttct aaaaatcttc tcttacttgc tggaacagga 480
tctttgtaga gcagcttgtg tatgtaaacg cttcagtgaa cttgctaatg atcccaattt 540
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<210> 32
<211> 197
<212> PRT
<213> Homo sapiens

<400> 32
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Arg Pro Arg Pro Val Gln Gln Gln Gln Gln Pro Pro Gln Gln Pro
  1               5                  10                  15

Pro Pro Gln Pro Pro Gln Gln Gln Pro Pro Gln Gln Gln Pro Pro Pro
             20                  25                  30

Pro Pro Gln Gln Gln Gln Gln Gln Pro Pro Pro Pro Pro Pro Pro
         35                  40                  45

Pro Pro Pro Leu Pro Gln Glu Arg Asn Asn Val Gly Glu Arg Asp Asp
     50                  55                  60

Asp Val Pro Ala Asp Met Val Ala Glu Glu Ser Gly Pro Gly Ala Gln
 65                  70                  75                  80

Asn Ser Pro Tyr Gln Leu Arg Arg Lys Thr Leu Leu Pro Lys Arg Thr
                 85                  90                  95

Ala Cys Pro Thr Lys Asn Ser Met Glu Gly Ala Ser Thr Ser Thr Thr
            100                 105                 110

Glu Asn Phe Gly His Arg Ala Lys Arg Ala Arg Val Ser Gly Lys Ser
        115                 120                 125

Gln Asp Leu Ser Ala Ala Pro Ala Glu Gln Tyr Leu Gln Glu Lys Leu
    130                 135                 140

Pro Asp Glu Val Val Leu Lys Ile Phe Ser Tyr Leu Leu Glu Gln Asp
```

```
145                 150                 155                 160

Leu Cys Arg Ala Ala Cys Val Cys Lys Arg Phe Ser Glu Leu Ala Asn
                165                 170                 175

Asp Pro Asn Leu Trp Lys Arg Leu Tyr Met Glu Val Phe Glu Tyr Thr
            180                 185                 190

Arg Pro Met Met His
        195
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<210> 33
<211> 537
<212> DNA
<213> Homo sapiens

<400> 33
gcggccgcgg cccggactcc gcggtgggcg agcgccctgt gaggtgacca tggaggctgg 60
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ccgctgcagc ctggtatgca gggcctggta tgaactgatc ctcagtctcg acagcacccg 180
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cttggccatg gccagcctgt atgaccgaat tgtgctcttc ccaggtgtgt acgaagagca 480
aggtgaaatc atcttgaagg tgcctgtgga gattgtaggg caggggaagt tgggtga 537

<210> 34
<211> 178
<212> PRT
<213> Homo sapiens

<400> 34
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Arg Pro Arg Pro Gly Leu Arg Gly Gly Arg Ala Pro Cys Glu Val Thr
  1               5                  10                  15

Met Glu Ala Gly Gly Leu Pro Leu Glu Leu Trp Arg Met Ile Leu Ala
             20                  25                  30

Tyr Leu His Leu Pro Asp Leu Gly Arg Cys Ser Leu Val Cys Arg Ala
         35                  40                  45

Trp Tyr Glu Leu Ile Leu Ser Leu Asp Ser Thr Arg Trp Arg Gln Leu
     50                  55                  60

Cys Leu Gly Cys Thr Glu Cys Arg His Pro Asn Trp Pro Asn Gln Pro
 65                  70                  75                  80

Asp Val Glu Pro Glu Ser Trp Arg Glu Ala Phe Lys Gln His Tyr Leu
                 85                  90                  95

Ala Ser Lys Thr Trp Thr Lys Asn Ala Leu Asp Leu Glu Ser Ser Ile
            100                 105                 110

Cys Phe Ser Leu Phe Arg Arg Arg Arg Glu Arg Arg Thr Leu Ser Val
        115                 120                 125

Gly Pro Gly Arg Glu Phe Asp Ser Leu Gly Ser Ala Leu Ala Met Ala
    130                 135                 140

Ser Leu Tyr Asp Arg Ile Val Leu Phe Pro Gly Val Tyr Glu Glu Gln
145                 150                 155                 160
```

```
Gly Glu Ile Ile Leu Lys Val Pro Val Glu Ile Val Gly Gln Gly Lys
                165                 170                 175

Leu Gly
```

<210> 35
<211> 751
<212> DNA
<213> Homo sapiens

<400> 35
gagaccgaga cggcgccgct gaccctagag tcgctgccca ccgatcccct gctcctcatc 60
ttatcctttt tggactatcg ggatctaatc aactgttgtt atgtcagtcg aagattaagc 120
cagctatcaa gtcatgatcc gctgtggaga agacattgca aaaaatactg gctgatatct 180
gaggaagaga aaacacagaa gaatcagtgt tggaaatctc tcttcataga tacttactct 240
gatgtaggaa gatacattga ccattatgct gctattaaaa aggcctcggg aatgatctca 300
agaaatattt ggagcccagg tgtcctcgga tgggttttat ctctgaaaga ggggtgctcg 360
agaggaagac ctcgatgctg tggaagcgca gattgggctg caagtttcct ggacgattat 420
cgatgttcat accgaattca caatggacag aagttagttg gttcctgggg ttattgggaa 480
gcatggcact gtctaatcac tatcgttctg aagatttgtt agacgtcgat acagctgccg 540
gagattccag cagagacagg gactgaaata ctgtctccct ttaacttttg catacatact 600
ggtttgagtc agtacatagc agtggaagct gcagagggtt gaaacaaaaa tgaagttttc 660
taccaatgtc agacagtaga acgtgtgttt aaatatggca ttaagatgtg ttctgatggt 720
tgtataaatg gcatgcatta ggtattttca g   751

<210> 36
<211> 247
<212> PRT
<213> Homo sapiens

<400> 36
```
Glu Thr Glu Thr Ala Pro Leu Thr Leu Glu Ser Leu Pro Thr Asp Pro
  1               5                  10                  15

Leu Leu Leu Ile Leu Ser Phe Leu Asp Tyr Arg Asp Leu Ile Asn Cys
             20                  25                  30

Cys Tyr Val Ser Arg Arg Leu Ser Gln Leu Ser Ser His Asp Pro Leu
         35                  40                  45

Trp Arg Arg His Cys Lys Lys Tyr Trp Leu Ile Ser Glu Glu Glu Lys
     50                  55                  60

Thr Gln Lys Asn Gln Cys Trp Lys Ser Leu Phe Ile Asp Thr Tyr Ser
 65                  70                  75                  80

Asp Val Gly Arg Tyr Ile Asp His Tyr Ala Ala Ile Lys Lys Ala Ser
                 85                  90                  95

Gly Met Ile Ser Arg Asn Ile Trp Ser Pro Gly Val Leu Gly Trp Val
            100                 105                 110

Leu Ser Leu Lys Glu Gly Cys Ser Arg Gly Arg Pro Arg Cys Cys Gly
        115                 120                 125

Ser Ala Asp Trp Ala Ala Ser Phe Leu Asp Asp Tyr Arg Cys Ser Tyr
    130                 135                 140

Arg Ile His Asn Gly Gln Lys Leu Val Gly Ser Trp Gly Tyr Trp Glu
145                 150                 155                 160
```

Ala Trp His Cys Leu Ile Thr Ile Val Leu Lys Ile Cys Thr Ser Ile
165 170 175

Gln Leu Pro Glu Ile Pro Ala Glu Thr Gly Thr Glu Ile Leu Ser Pro
180 185 190

Phe Asn Phe Cys Ile His Thr Gly Leu Ser Gln Tyr Ile Ala Val Glu
195 200 205

Ala Ala Glu Gly Asn Lys Asn Glu Val Phe Tyr Gln Cys Gln Thr Val
210 215 220

Glu Arg Val Phe Lys Tyr Gly Ile Lys Met Cys Ser Asp Gly Cys Ile
225 230 235 240

Asn Gly Met His Val Phe Ser
245

<210> 37
<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> all n positions
<223> n=a, c, g or t

<400> 37
ggctccggtt tccgggccgg cgggtggccg ctcaccatgc ccggnaagca ccagcatttc 60
caggaacctg aggtcggctg ctgcgggaaa tacttcctgt ttggcttcaa cattgtcttc 120
tgggtgctgg gagccctgtt cctggctatc ggcctctggg cctggggtga gaagggcgtt 180
ctctcgaaca tctcagcgct gacagatctg ggaggccttg accccgtgtg gcttgtttgt 240
ggtagttgga ggcgtcatgt cggtgctggg ctttgctggg ctgcaattgg ggccctccgg 300
gagaacacct tcctgctcaa gtttttctnc gngttcctcg gtctcatctt cttcctggag 360
ctggcaac 368

<210> 38
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> all Xaa positions
<223> Xaa=unknown amino acid residue

<400> 38
Gly Ser Gly Phe Arg Ala Gly Gly Trp Pro Leu Thr Met Pro Gly Lys
1 5 10 15

His Gln His Phe Gln Glu Pro Glu Val Gly Cys Cys Gly Lys Tyr Phe
20 25 30

Leu Phe Gly Phe Asn Ile Val Phe Trp Val Leu Gly Ala Leu Phe Leu
35 40 45

Ala Ile Gly Leu Trp Ala Trp Gly Glu Lys Gly Val Leu Ser Asn Ile
50 55 60

Ser Ala Leu Thr Asp Leu Gly Gly Leu Asp Pro Val Trp Leu Val Cys
65 70 75 80

Gly Ser Trp Arg Arg His Val Gly Ala Gly Leu Cys Trp Ala Ala Ile
85 90 95

Gly Ala Leu Arg Glu Asn Thr Phe Leu Leu Lys Phe Phe Xaa Xaa Phe
100 105 110

Leu Gly Leu Ile Phe Phe Leu Glu Leu Ala
115 120

<210> 39
<211> 774
<212> DNA
<213> Homo sapiens

<400> 39
gcggcggccg ccgccgcgta cctggacgag ctgcccgagc cgctgctgct gcgcgtgctg 60
gccgcactgc cggccgccga gctggtgcag gcctgccgcc tggtgtgcct gcgctggaag 120
gagctggtgg acggcgcccc gctgtggctg ctcaagtgcc agcaggaggg gctggtgccc 180
gagggcggcg tggaggagga gcgcgaccac tggcagcagt tctacttcct gagcaagcgg 240
cgccgcaacc ttctgcgtaa cccgtgtggg gaagaggact tggaaggctg gtgtgacgtg 300
gagcatggtg gggacggctg gaggggtgag gagctgcctg gagacagtgg ggtggagttc 360
acccacgatg agagcgtcaa gaagtacttc gcctcctcct ttgagtggtg tcgcaaagca 420
caggtcattg acctgcaggc tgagggctac tgggaggagc tgctggacac gactcagccg 480
gccatcgtgg tgaaggactg gtactcgggc cgcagcgacg ctggttgcct ctacgagctc 540
accgttaagc tactgtccga gcacgagaac gtgctggctg agttcagcag cgggcaggtg 600
gcagtgcccc aagacagtga cggcgggggc tggatggaga tctcccacac cttcaccgac 660
tacgggccgg gcgtccgctt cgtccgcttc gagcacgggg ggcagggctc cgtctactgg 720
aagggctggt tcggggcccg ggtgaccaac agcagcgtgt gggtagaacc ctga 774

<210> 40
<211> 257
<212> PRT
<213> Homo sapiens

<400> 40
Ala Ala Ala Ala Ala Ala Tyr Leu Asp Glu Leu Pro Glu Pro Leu Leu
1 5 10 15

Leu Arg Val Leu Ala Ala Leu Pro Ala Ala Glu Leu Val Gln Ala Cys
20 25 30

Arg Leu Val Cys Leu Arg Trp Lys Glu Leu Val Asp Gly Ala Pro Leu
35 40 45

Trp Leu Leu Lys Cys Gln Gln Glu Gly Leu Val Pro Glu Gly Gly Val
50 55 60

Glu Glu Glu Arg Asp His Trp Gln Gln Phe Tyr Phe Leu Ser Lys Arg
65 70 75 80

Arg Arg Asn Leu Leu Arg Asn Pro Cys Gly Glu Glu Asp Leu Glu Gly
85 90 95

Trp Cys Asp Val Glu His Gly Gly Asp Gly Trp Arg Val Glu Glu Leu
100 105 110

Pro Gly Asp Ser Gly Val Glu Phe Thr His Asp Glu Ser Val Lys Lys
115 120 125

Tyr Phe Ala Ser Ser Phe Glu Trp Cys Arg Lys Ala Gln Val Ile Asp
130 135 140

```
Leu Gln Ala Glu Gly Tyr Trp Glu Glu Leu Leu Asp Thr Thr Gln Pro
145                 150                 155                 160

Ala Ile Val Val Lys Asp Trp Tyr Ser Gly Arg Ser Asp Ala Gly Cys
                165                 170                 175

Leu Tyr Glu Leu Thr Val Lys Leu Leu Ser Glu His Glu Asn Val Leu
            180                 185                 190

Ala Glu Phe Ser Ser Gly Gln Val Ala Val Pro Gln Asp Ser Asp Gly
        195                 200                 205

Gly Gly Trp Met Glu Ile Ser His Thr Phe Thr Asp Tyr Gly Pro Gly
    210                 215                 220

Val Arg Phe Val Arg Phe Glu His Gly Gly Gln Gly Ser Val Tyr Trp
225                 230                 235                 240

Lys Gly Trp Phe Gly Ala Arg Val Thr Asn Ser Ser Val Trp Val Glu
                245                 250                 255

Pro
```

<210> 41
<211> 957
<212> DNA
<213> Homo sapiens

<400> 41
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atgggcgaga aggcggtccc tttgctaagg aggaggcggg tgaagagaag ctgcccttct 60
tgtggctcgg agcttggggt tgaagagaag aggggaaaag gaaatccgat ttccatccag 120
ttgttccccc cagagctggt ggagcatatc atctcattcc tcccagtcag agaccttgtt 180
gccctcggcc agacctgccg ctacttccac gaagtgtgcg atggggaagg cgtgtggaga 240
cgcatctgtc gcagactcag tccgcgcctc caagatcagg acacgaaggg cctgtatttc 300
caggcatttg gaggccgccg ccgatgtctc agcaagagcg tggcccctt gctagcccac 360
ggctaccgcc gcttcttgcc caccaaggat cacgtcttca ttcttgacta cgtggggacc 420
ctcttcttcc tcaaaaatgc cctggtctcc accctcggcc agatgcagtg gaagcgggcc 480
tgtcgctatg ttgtgttgtg tcgtggagcc aaggattttg cctcggaccc aaggtgtgac 540
acagtttacc gtaaatacct ctacgtcttg gccactcggg agccgcagga agtggtgggt 600
accaccagca gccgggcctg tgactgtgtt gaggtctatc tgcagtctag tgggcagcgg 660
gtcttcaaga tgacattcca ccactcaatg accttcaagc agatcgtgct ggttggtcag 720
gagacccagc gggctctact gctcctcaca gaggaaggaa agatctactc tttggtagtg 780
aatgagaccc agcttgacca gccacgctcc tacacggttc agctggccct gaggaaggtg 840
tcccactacc tgcctcacct gcgcgtggcc tgcatgactt ccaaccagag cagcaccctc 900
tacgtcacag atcctattct gtgctcttgg ctacaaccac cttggcctgg tggatga    957
```

<210> 42
<211> 318
<212> PRT
<213> Homo sapiens

<400> 42
```
Met Gly Glu Lys Ala Val Pro Leu Leu Arg Arg Arg Arg Val Lys Arg
  1               5                  10                  15

Ser Cys Pro Ser Cys Gly Ser Glu Leu Gly Val Glu Glu Lys Arg Gly
            20                  25                  30

Lys Gly Asn Pro Ile Ser Ile Gln Leu Phe Pro Pro Glu Leu Val Glu
        35                  40                  45
```

```
His Ile Ile Ser Phe Leu Pro Val Arg Asp Leu Val Ala Leu Gly Gln
 50                  55                  60

Thr Cys Arg Tyr Phe His Glu Val Cys Asp Gly Glu Gly Val Trp Arg
 65                  70                  75                  80

Arg Ile Cys Arg Arg Leu Ser Pro Arg Leu Gln Asp Gln Asp Thr Lys
                 85                  90                  95

Gly Leu Tyr Phe Gln Ala Phe Gly Gly Arg Arg Arg Cys Leu Ser Lys
            100                 105                 110

Ser Val Ala Pro Leu Leu Ala His Gly Tyr Arg Arg Phe Leu Pro Thr
        115                 120                 125

Lys Asp His Val Phe Ile Leu Asp Tyr Val Gly Thr Leu Phe Phe Leu
    130                 135                 140

Lys Asn Ala Leu Val Ser Thr Leu Gly Gln Met Gln Trp Lys Arg Ala
145                 150                 155                 160

Cys Arg Tyr Val Val Leu Cys Arg Gly Ala Lys Asp Phe Ala Ser Asp
                165                 170                 175

Pro Arg Cys Asp Thr Val Tyr Arg Lys Tyr Leu Tyr Val Leu Ala Thr
            180                 185                 190

Arg Glu Pro Gln Glu Val Val Gly Thr Thr Ser Ser Arg Ala Cys Asp
        195                 200                 205

Cys Val Glu Val Tyr Leu Gln Ser Ser Gly Gln Arg Val Phe Lys Met
    210                 215                 220

Thr Phe His His Ser Met Thr Phe Lys Gln Ile Val Leu Val Gly Gln
225                 230                 235                 240

Glu Thr Gln Arg Ala Leu Leu Leu Leu Thr Glu Glu Gly Lys Ile Tyr
                245                 250                 255

Ser Leu Val Val Asn Glu Thr Gln Leu Asp Gln Pro Arg Ser Tyr Thr
            260                 265                 270

Val Gln Leu Ala Leu Arg Lys Val Ser His Tyr Leu Pro His Leu Arg
        275                 280                 285

Val Ala Cys Met Thr Ser Asn Gln Ser Ser Thr Leu Tyr Val Thr Asp
    290                 295                 300

Pro Ile Leu Cys Ser Trp Leu Gln Pro Pro Trp Pro Gly Gly
305                 310                 315
```

<210> 43
<211> 1590
<212> DNA
<213> Homo sapiens

<400> 43
cgaggggaa gcgaaggaag gggaagagga agggaaaagc gagcgagagg ggcaaggcgg 60
aagaggaagc agggcggaag ggaagcccgg gccgcagacg gcgaaggagg cagcgggccg 120
ggggctgagg cgggagcgag gacacgccca agagaggaag cagagggagg cggaagcgtg 180
gaggaagggg cgagaggcat catcaaagga gatgagggga gcgtaggggc cgggaaagag 240
gcacaaggaa gaaagtatgg gaaggaggaa tggagggtca gggctaggcg gcgggagggc 300

gccaggccgg gaagagtaca aggacaagga ggtcaggttt gggcctacat cccggggaca 360
ggggcggcca tggcggcggc agccagggag gaggaggagg aggcggctcg ggagtcagcc 420
gcctgcccgg ctgcggggcc agcgctctgg cgcctgccgg aagtgtgctg gctgcacatg 480
tgctcctacc tcgacatgcg ggccctcggc cgcctggccc aggtgtaccg ctggctgtgg 540
cacttcacca actgcgacct gctccggcgc cagatagcct gggcctcgct caactccggc 600
ttcacgcggc tcggcaccaa cctgatgacc agtgtcccag tgaaggtgtc tcagaactgg 660
atagtggggt gctgccgaga ggggattctg ctgaagtgga gatgcagtca gatgccctgg 720
atgcagctag aggatgatgc tttgtacata tcccaggcta atttcatcct ggcctaccag 780
ttccgtccag atggtgccag cttgaaccgt cagcctctgg gagtctctgc tgggcatgat 840
gaggacgttt gccactttgt gctggccacc tcgcatattg tcagtgcagg aggagatggg 900
aagattggcc ttggtaagat tcacagcacc ttcgctgcca agtactgggc tcatgaacag 960
gaggtgaact gtgtggattg caaagggggc atcatatcat ttggctccag ggacaggacg 1020
gccaaggtgt ggcctttggc ctcaggccag ctggggcagt gtttatacac catccagact 1080
gaagaccaaa tctggtctgt tgctatcagg ccattactca gctcttttgt gacagggacg 1140
gcttgttgtg ggcacttctc acccctgaaa atctgggacc tcaacagtgg gcagctgatg 1200
acacacttgg acagagactt tcccccaagg gctggggtgc tggatgtcat atatgagtcc 1260
cctttcgcac tgctctcctg tggctatgac acctatgttc gctactggga ctgccgcacc 1320
agtgtccgga aatgtgtcat ggagtgggag gagccccaca acagcaccct gtactgcctg 1380
cagacagatg gcaaccactt gcttgccaca ggttcctcct tctatagcgt tgtacggctg 1440
tgggaccggc accaaagggc ctgcccgcac accttcccgc tgacgtcgac ccgcctcggc 1500
agccctgtgt actgcctgca tctcaccacc aagcatctct atgctgcgct gtcttacaac 1560
ctccacgtcc tggatattca aaacccgtga 1590

<210> 44
<211> 529
<212> PRT
<213> Homo sapiens

<400> 44
Arg Gly Gly Ser Glu Gly Arg Gly Arg Gly Arg Glu Lys Arg Ala Arg
1 5 10 15

Gly Ala Arg Arg Lys Arg Lys Gln Gly Gly Arg Glu Ala Arg Ala Ala
20 25 30

Asp Gly Glu Gly Gly Ser Gly Pro Gly Ala Glu Ala Gly Ala Arg Thr
35 40 45

Arg Pro Arg Glu Glu Ala Glu Gly Gly Gly Ser Val Glu Glu Gly Ala
50 55 60

Arg Gly Ile Ile Lys Gly Asp Glu Gly Ser Val Gly Ala Gly Lys Glu
65 70 75 80

Ala Gln Gly Arg Lys Tyr Gly Lys Glu Glu Trp Arg Val Arg Ala Arg
85 90 95

Arg Arg Glu Gly Ala Arg Pro Gly Arg Val Gln Gly Gln Gly Gly Gln
100 105 110

Val Trp Ala Tyr Ile Pro Gly Thr Gly Ala Ala Met Ala Ala Ala Ala
115 120 125

Arg Glu Glu Glu Glu Glu Ala Ala Arg Glu Ser Ala Ala Cys Pro Ala
130 135 140

Ala Gly Pro Ala Leu Trp Arg Leu Pro Glu Val Leu Leu Leu His Met
145 150 155 160

Cys Ser Tyr Leu Asp Met Arg Ala Leu Gly Arg Leu Ala Gln Val Tyr
165 170 175

Arg Trp Leu Trp His Phe Thr Asn Cys Asp Leu Leu Arg Arg Gln Ile

```
                180                 185                 190
Ala Trp Ala Ser Leu Asn Ser Gly Phe Thr Arg Leu Gly Thr Asn Leu
        195                 200                 205
Met Thr Ser Val Pro Val Lys Val Ser Gln Asn Trp Ile Val Gly Cys
    210                 215                 220
Cys Arg Glu Gly Ile Leu Leu Lys Trp Arg Cys Ser Gln Met Pro Trp
225                 230                 235                 240
Met Gln Leu Glu Asp Asp Ala Leu Tyr Ile Ser Gln Ala Asn Phe Ile
                245                 250                 255
Leu Ala Tyr Gln Phe Arg Pro Asp Gly Ala Ser Leu Asn Arg Gln Pro
            260                 265                 270
Leu Gly Val Ser Ala Gly His Asp Glu Asp Val Cys His Phe Val Leu
        275                 280                 285
Ala Thr Ser His Ile Val Ser Ala Gly Gly Asp Gly Lys Ile Gly Leu
    290                 295                 300
Gly Lys Ile His Ser Thr Phe Ala Ala Lys Tyr Trp Ala His Glu Gln
305                 310                 315                 320
Glu Val Asn Cys Val Asp Cys Lys Gly Gly Ile Ile Ser Phe Gly Ser
                325                 330                 335
Arg Asp Arg Thr Ala Lys Val Trp Pro Leu Ala Ser Gly Gln Leu Gly
            340                 345                 350
Gln Cys Leu Tyr Thr Ile Gln Thr Glu Asp Gln Ile Trp Ser Val Ala
        355                 360                 365
Ile Arg Pro Leu Leu Ser Ser Phe Val Thr Gly Thr Ala Cys Cys Gly
    370                 375                 380
His Phe Ser Pro Leu Lys Ile Trp Asp Leu Asn Ser Gly Gln Leu Met
385                 390                 395                 400
Thr His Leu Asp Arg Asp Phe Pro Pro Arg Ala Gly Val Leu Asp Val
                405                 410                 415
Ile Tyr Glu Ser Pro Phe Ala Leu Leu Ser Cys Gly Tyr Asp Thr Tyr
            420                 425                 430
Val Arg Tyr Trp Asp Cys Arg Thr Ser Val Arg Lys Cys Val Met Glu
        435                 440                 445
Trp Glu Glu Pro His Asn Ser Thr Leu Tyr Cys Leu Gln Thr Asp Gly
    450                 455                 460
Asn His Leu Leu Ala Thr Gly Ser Ser Phe Tyr Ser Val Val Arg Leu
465                 470                 475                 480
Trp Asp Arg His Gln Arg Ala Cys Pro His Thr Phe Pro Leu Thr Ser
                485                 490                 495
Thr Arg Leu Gly Ser Pro Val Tyr Cys Leu His Leu Thr Thr Lys His
            500                 505                 510
Leu Tyr Ala Ala Leu Ser Tyr Asn Leu His Val Leu Asp Ile Gln Asn
```

515 520 525

Pro

<210> 45
<211> 1214
<212> DNA
<213> Homo sapiens

<400> 45
gcattgctat aattttacta tactctcatc taaatctaaa atcagtcttc aaaataaaaa 60
caaattgtcc tttgccaaaa attttttaa tcgcacaatt aattgacatt aactgccaat 120
tctttttggc taattgacta attttaactt ctgtgttgct tttccagagg catggctatt 180
gcaccttggg agaagccttt aatcggttag acttctcaag tgcaattcaa gatatccgaa 240
cgttcaatta tgtggtcaaa ctgttgcagc taattgcaaa atcccagtta acttcattga 300
gtggcgtggc acagaagaat tacttcaaca ttttggataa aatcgttcaa aaggttcttg 360
atgaccacca caatcctcgc ttaatcaaag atcttctgca agacctaagc tctaccctct 420
gcattcttat tagaggagta gggaagtctg tattagtggg aaacatcaat atttggattt 480
gccgattaga aactattctc gcctggcaac aacagctaca ggatcttcag atgactaagc 540
aagtgaacaa tggcctcacc ctcagtgacc ttcctctgca catgctgaac aacatcctat 600
accggttctc agacggatgg gacatcatca ccttaggcca ggtgaccccc acgttgtata 660
tgcttagtga agacagacag ctgtggaaga agctttgtca gtaccatttt gctgaaaagc 720
agttttgtag acatttgatc ctttcagaaa aaggtcatat tgaatggaag ttgatgtact 780
ttgcacttca gaaacattac ccagcgaagg agcagtacgg agacacactg catttctgtc 840
ggcactgcag cattctcttt tggaaggact caggacaccc ctgcacggcg gccgaccctg 900
acagctgctt cacgcctgtg tctccgcagc acttcatcga cctcttcaag ttttaagggc 960
tgcccctgcc atcctattg gagattgtga atcctgctgt ctgtgcaggg ctcatagtga 1020
gtgttctgtg aggtgggtgg agactcctcg gaagcccctg cttccagaaa gcctgggaag 1080
aactgccctt ctgcaaaggg gggactgcat ggttgcattt tcatcactga aagtcagagg 1140
ccaaggaaat catttctact tctttaaaaa ctccttctaa gcatattaaa atgtgaaatt 1200
ttgcgtactc tctc 1214

<210> 46
<211> 272
<212> PRT
<213> Homo sapiens

<400> 46
Leu Ile Leu Thr Ser Val Leu Leu Phe Gln Arg His Gly Tyr Cys Thr
1 5 10 15

Leu Gly Glu Ala Phe Asn Arg Leu Asp Phe Ser Ser Ala Ile Gln Asp
20 25 30

Ile Arg Thr Phe Asn Tyr Val Val Lys Leu Leu Gln Leu Ile Ala Lys
35 40 45

Ser Gln Leu Thr Ser Leu Ser Gly Val Ala Gln Lys Asn Tyr Phe Asn
50 55 60

Ile Leu Asp Lys Ile Val Gln Lys Val Leu Asp Asp His His Asn Pro
65 70 75 80

Arg Leu Ile Lys Asp Leu Leu Gln Asp Leu Ser Ser Thr Leu Cys Ile
85 90 95

Leu Ile Arg Gly Val Gly Lys Ser Val Leu Val Gly Asn Ile Asn Ile
100 105 110

Trp Ile Cys Arg Leu Glu Thr Ile Leu Ala Trp Gln Gln Gln Leu Gln
115 120 125

```
Asp Leu Gln Met Thr Lys Gln Val Asn Asn Gly Leu Thr Leu Ser Asp
   130                 135                 140

Leu Pro Leu His Met Leu Asn Asn Ile Leu Tyr Arg Phe Ser Asp Gly
145                 150                 155                 160

Trp Asp Ile Ile Thr Leu Gly Gln Val Thr Pro Thr Leu Tyr Met Leu
                165                 170                 175

Ser Glu Asp Arg Gln Leu Trp Lys Lys Leu Cys Gln Tyr His Phe Ala
            180                 185                 190

Glu Lys Gln Phe Cys Arg His Leu Ile Leu Ser Glu Lys Gly His Ile
        195                 200                 205

Glu Trp Lys Leu Met Tyr Phe Ala Leu Gln Lys His Tyr Pro Ala Lys
    210                 215                 220

Glu Gln Tyr Gly Asp Thr Leu His Phe Cys Arg His Cys Ser Ile Leu
225                 230                 235                 240

Phe Trp Lys Asp Ser Gly His Pro Cys Thr Ala Ala Asp Pro Asp Ser
                245                 250                 255

Cys Phe Thr Pro Val Ser Pro Gln His Phe Ile Asp Leu Phe Lys Phe
            260                 265                 270
```

<210> 47
<211> 4059
<212> DNA
<213> Homo sapiens

<400> 47
agtacggcag tgagggcaaa ggcagctcga gcatctcatc tgacgtgagt tcaagtacag 60
atcacacgcc cactaaagcc cagaagaatg tggctaccag cgaagactcc gacctgagca 120
tgcgcacact gagcacgccc agcccagccc tgatatgtcc accgaatctc ccaggatttc 180
agaatggaag gggctcgtcc acctcctcgt cctccatcac cggggagacg gtggccatgg 240
tgcactcccc gcccccgacc cgcctcacac acccgctcat ccggctcgcc tccagacccc 300
agaaggagca ggccagcata gaccggctcc cggaccactc catggtgcag atcttctcct 360
tcctgcccac caaccagctg tgccgctgcg cgcgagtgtg ccgccgctgg tacaacctgg 420
cctgggaccc gcggctctgg aggactatcc gcctgacggg cgagaccatc aacgtggacc 480
gcgccctcaa ggtgctgacc cgcagactct gccaggacac ccccaacgtg tgtctcatgc 540
tggaaaccgt aactgtcagt ggctgcaggc ggctcacaga ccgagggctg tacaccatcg 600
cccagtgctg ccccgaactg aggcgactgg aagtctcagg ctgttacaat atctccaacg 660
aggccgtctt tgatgtggtg tccctctgcc ctaatctgga gcacctggat gtgtcaggat 720
gctccaaagt gacctgcatc agcttgaccc gggaggcctc cattaaactg tcaccttgc 780
atggcaaaca gatttccatc cgctacctgg acatgacgga ctgcttcgtg ctggaggacg 840
aaggcctgca caccatcgcg gcgcactgca cgcagctcac ccacctctac ctgcgccgct 900
gcgtccgcct gaccgacgaa ggcctgcgct acctggtgat ctactgcgcc tccatcaagg 960
agctgagcgt cagcgactgc cgcttcgtca gcgacttcgg cctgcgggag atcgccaagc 1020
tggagtcccg cctgcggtac ctgagcatcg cgcactgcgg ccgggtcacc gacgtgggca 1080
tccgctacgt ggccaagtac tgcagcaagc tgcgctacct caacgcgagg ggctgcgagg 1140
gcatcacgga ccacggtgtg gagtacctcg ccaagaactg caccaaactc aaatccctgg 1200
atatcggcaa atgccctttg gtatccgaca cgggcctgga gtgcctggcc ctgaactgct 1260
tcaacctcaa gcggctcagc ctcaagtcct gcgagagcat caccggccag ggcttgcaga 1320
tcgtggccgc caactgcttt gacctccaga cgctgaatgt ccaggactgc gaggtctccg 1380
tggaggccct gcgctttgtc aaacgccact gcaagcgctg cgtcatcgag cacaccaacc 1440
cggctttctt ctgaagggac agagttcatc cggcgttgta ttcacacaaa cctgaacaaa 1500
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tccgggaagg ttattaggaa tctggccttt atttttcctc atttctcatg ggcaacagag 1620
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<210> 48
<211> 483
<212> PRT
<213> Homo sapiens

<400> 48
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20 25 30

Ser Glu Asp Ser Asp Leu Ser Met Arg Thr Leu Ser Thr Pro Ser Pro
35 40 45

Ala Leu Ile Cys Pro Pro Asn Leu Pro Gly Phe Gln Asn Gly Arg Gly
50 55 60

Ser Ser Thr Ser Ser Ser Ser Ile Thr Gly Glu Thr Val Ala Met Val
65 70 75 80

```
His Ser Pro Pro Pro Thr Arg Leu Thr His Pro Leu Ile Arg Leu Ala
                 85                  90                  95

Ser Arg Pro Gln Lys Glu Gln Ala Ser Ile Asp Arg Leu Pro Asp His
            100                 105                 110

Ser Met Val Gln Ile Phe Ser Phe Leu Pro Thr Asn Gln Leu Cys Arg
        115                 120                 125

Cys Ala Arg Val Cys Arg Arg Trp Tyr Asn Leu Ala Trp Asp Pro Arg
    130                 135                 140

Leu Trp Arg Thr Ile Arg Leu Thr Gly Glu Thr Ile Asn Val Asp Arg
145                 150                 155                 160

Ala Leu Lys Val Leu Thr Arg Arg Leu Cys Gln Asp Thr Pro Asn Val
                165                 170                 175

Cys Leu Met Leu Glu Thr Val Thr Val Ser Gly Cys Arg Arg Leu Thr
            180                 185                 190

Asp Arg Gly Leu Tyr Thr Ile Ala Gln Cys Cys Pro Glu Leu Arg Arg
        195                 200                 205

Leu Glu Val Ser Gly Cys Tyr Asn Ile Ser Asn Glu Ala Val Phe Asp
    210                 215                 220

Val Val Ser Leu Cys Pro Asn Leu Glu His Leu Asp Val Ser Gly Cys
225                 230                 235                 240

Ser Lys Val Thr Cys Ile Ser Leu Thr Arg Glu Ala Ser Ile Lys Leu
                245                 250                 255

Ser Pro Leu His Gly Lys Gln Ile Ser Ile Arg Tyr Leu Asp Met Thr
            260                 265                 270

Asp Cys Phe Val Leu Glu Asp Glu Gly Leu His Thr Ile Ala Ala His
        275                 280                 285

Cys Thr Gln Leu Thr His Leu Tyr Leu Arg Arg Cys Val Arg Leu Thr
    290                 295                 300

Asp Glu Gly Leu Arg Tyr Leu Val Ile Tyr Cys Ala Ser Ile Lys Glu
305                 310                 315                 320

Leu Ser Val Ser Asp Cys Arg Phe Val Ser Asp Phe Gly Leu Arg Glu
                325                 330                 335

Ile Ala Lys Leu Glu Ser Arg Leu Arg Tyr Leu Ser Ile Ala His Cys
            340                 345                 350

Gly Arg Val Thr Asp Val Gly Ile Arg Tyr Val Ala Lys Tyr Cys Ser
        355                 360                 365

Lys Leu Arg Tyr Leu Asn Ala Arg Gly Cys Glu Gly Ile Thr Asp His
    370                 375                 380

Gly Val Glu Tyr Leu Ala Lys Asn Cys Thr Lys Leu Lys Ser Leu Asp
385                 390                 395                 400

Ile Gly Lys Cys Pro Leu Val Ser Asp Thr Gly Leu Glu Cys Leu Ala
                405                 410                 415
```

```
Leu Asn Cys Phe Asn Leu Lys Arg Leu Ser Leu Lys Ser Cys Glu Ser
        420                 425                 430

Ile Thr Gly Gln Gly Leu Gln Ile Val Ala Ala Asn Cys Phe Asp Leu
    435                 440                 445

Gln Thr Leu Asn Val Gln Asp Cys Glu Val Ser Val Glu Ala Leu Arg
450                 455                 460

Phe Val Lys Arg His Cys Lys Arg Cys Val Ile Glu His Thr Asn Pro
465                 470                 475                 480

Ala Phe Phe
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<210> 49
<211> 850
<212> DNA
<213> Homo sapiens

<400> 49
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ggcggacggc cccatgccct tcctgggcag ggctgcgcgc gtgtgccgcc gctggcagga 180
ggccgcttcc caacccgcgc tctggcacac cgtgaccctg tcgtccccgc tggtcggccg 240
gcctgccaag ggcggggtca aggcggagaa gaagctcctt gcttccctgg agtggcttat 300
gcccaatcgg ttttcacagc tccagaggct gaccctcatc cactggaagt ctcaggtaca 360
ccccgtgttg aagctggtag gtgagtgctg tcctcggctc actttcctca agctctccgg 420
ctgccacggt gtgactgctg acgctctggt catgctagcc aaagcctgct gccagctcca 480
tagcctggac ctacagcact ccatggtgga gtccacagct gtggtgagct tcttggagga 540
ggcagggtcc cgaatgcgca agttgtggct gacctacagc tcccagacga cagccatcct 600
gggcgcattg ctgggcagct gctgccccca gctccaggtc ctggaggtga gcaccggcat 660
caaccgtaat agcattcccc ttcagctgcc tgtcgaggct ctgcagaaag gctgccctca 720
gctccaggtg ctgcggctgt tgaacctgat gtggctgccc aagcctccgg gacgaggggt 780
ggctcccgga ccaggcttcc ctagcctaga ggagctctgc ctggcgagct caacctgcaa 840
ctttgtgagc   850

<210> 50
<211> 283
<212> PRT
<213> Homo sapiens

<400> 50
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Ala Ala Ala Pro Ala Pro Ala Pro Ala Pro Thr Pro Thr Pro Glu Glu
  1               5                  10                  15

Gly Pro Asp Ala Gly Trp Gly Asp Arg Ile Pro Leu Glu Ile Leu Val
            20                  25                  30

Gln Ile Phe Gly Leu Leu Val Ala Ala Asp Gly Pro Met Pro Phe Leu
        35                  40                  45

Gly Arg Ala Ala Arg Val Cys Arg Arg Trp Gln Glu Ala Ala Ser Gln
    50                  55                  60

Pro Ala Leu Trp His Thr Val Thr Leu Ser Ser Pro Leu Val Gly Arg
65                  70                  75                  80

Pro Ala Lys Gly Gly Val Lys Ala Glu Lys Lys Leu Leu Ala Ser Leu
                85                  90                  95

Glu Trp Leu Met Pro Asn Arg Phe Ser Gln Leu Gln Arg Leu Thr Leu
```

```
            100                 105                 110

Ile His Trp Lys Ser Gln Val His Pro Val Leu Lys Leu Val Gly Glu
        115                 120                 125

Cys Cys Pro Arg Leu Thr Phe Leu Lys Leu Ser Gly Cys His Gly Val
    130                 135                 140

Thr Ala Asp Ala Leu Val Met Leu Ala Lys Ala Cys Cys Gln Leu His
145                 150                 155                 160

Ser Leu Asp Leu Gln His Ser Met Val Glu Ser Thr Ala Val Val Ser
                165                 170                 175

Phe Leu Glu Glu Ala Gly Ser Arg Met Arg Lys Leu Trp Leu Thr Tyr
            180                 185                 190

Ser Ser Gln Thr Thr Ala Ile Leu Gly Ala Leu Leu Gly Ser Cys Cys
        195                 200                 205

Pro Gln Leu Gln Val Leu Glu Val Ser Thr Gly Ile Asn Arg Asn Ser
    210                 215                 220

Ile Pro Leu Gln Leu Pro Val Glu Ala Leu Gln Lys Gly Cys Pro Gln
225                 230                 235                 240

Leu Gln Val Leu Arg Leu Leu Asn Leu Met Trp Leu Pro Lys Pro Pro
                245                 250                 255

Gly Arg Gly Val Ala Pro Gly Pro Gly Phe Pro Ser Leu Glu Glu Leu
            260                 265                 270

Cys Leu Ala Ser Ser Thr Cys Asn Phe Val Ser
        275                 280
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<210> 51
<211> 1777
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> all n positions
<223> n=a, c, g or t

<400> 51
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agaagtgtca gaacactcca caggtataac ccatcttcct cctgaggtaa tgctgtcaat 180
tttcagctat cttaatcctc aagagttatg tcgatgcagt caagtaagca tgaaatggtc 240
tcagctgaca aaaacgggat cgctttggaa acatctttac cctgttcatt gggccagagg 300
tgactggtat agtggtcccg caactgaact tgatactgaa cctgatgatg aatgggtgaa 360
aaataggaaa gatgaaagtc gtgcttttca tgagtgggat gaagatgctg acattgatga 420
atctgaagag tctgcggagg aatcaattgc tatcagcatt gcacaaatgg aaaaacgttt 480
actccatggc ttaattcata acgttctacc atatgttggt acttctgtaa aaaccttagt 540
attagcatac agctctgcag tttccagcaa aatggttagg cagattttag agctttgtcc 600
taacctggag catctggatc ttacccagac tgacatttca gattctgcat ttgacagttg 660
gtcttggctt ggttgctgcc agagtcttcg gcatcttgat ctgtctggtt gtgagaaaat 720
cacagatgtg gccctagaga agatttccag agctcttgga attctgacat ctcatcaaag 780
tggctttttg aaaacatcta caagcaaaat tacttcaact gcgtggaaaa ataaagacat 840
taccatgcag tccaccaagc agtatgcctg tttgcacgat ttaactaaca agggcattgg 900
agaagaaata gataatgaac acccctggac taagcctgtt tcttctgaga atttcacttc 960

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tccttatgtg tggatgttag atgctgaaga tttggctgat attgaagata ctgtggaatg 1020
gagacataga aatgttgaaa gtctttgtgt aatggaaaca gcatccaact ttagttgttc 1080
cacctctggt tgttttagta aggacattgt tggactaagg actagtgtct gttggcagca 1140
gcattgtgct tctccagcct ttgcgtattg tggtcactca ttttgttgta caggaacagc 1200
tttaagaact atgtcatcac tcccagaatc ttctgcaatg tgtagaaaag cagcaaggac 1260
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cagggttttg actctgggag gagggctgcc ttatttggag caccttaatc tctctggttg 1440
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tgaatacttt tactactgtg acaacattaa cggtcctcat gctgataccg ccagtggatg 1560
ccagaatttg cagtgtggtt ttcgagcctg ctgccgctct ggcgaatgac ccttgacttc 1620
tgatctttgt ctacttcatt tagctgagca ggctttcttt catgcacttt actcatagca 1680
catttcttgt gttaaccatc ccttttgag cgtgacttgt tttgggccca ttnyttacaa 1740
cttcagaaat cttaattacc agtgrattgt aatgttg                          1777
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<210> 52
<211> 590
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> all Xaa positions
<223> Xaa=unknown amino acid residue

<400> 52

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Gln His Cys Ser Gln Lys Asp Thr Ala Glu Leu Leu Arg Gly Leu Ser
  1               5                  10                  15

Leu Trp Asn His Ala Glu Glu Arg Gln Lys Phe Phe Lys Tyr Ser Val
             20                  25                  30

Asp Glu Lys Ser Asp Lys Glu Ala Glu Val Ser Glu His Ser Thr Gly
         35                  40                  45

Ile Thr His Leu Pro Pro Glu Val Met Leu Ser Ile Phe Ser Tyr Leu
     50                  55                  60

Asn Pro Gln Glu Leu Cys Arg Cys Ser Gln Val Ser Met Lys Trp Ser
 65                  70                  75                  80

Gln Leu Thr Lys Thr Gly Ser Leu Trp Lys His Leu Tyr Pro Val His
                 85                  90                  95

Trp Ala Arg Gly Asp Trp Tyr Ser Gly Pro Ala Thr Glu Leu Asp Thr
            100                 105                 110

Glu Pro Asp Asp Glu Trp Val Lys Asn Arg Lys Asp Glu Ser Arg Ala
        115                 120                 125

Phe His Glu Trp Asp Glu Asp Ala Asp Ile Asp Glu Ser Glu Glu Ser
    130                 135                 140

Ala Glu Glu Ser Ile Ala Ile Ser Ile Ala Gln Met Glu Lys Arg Leu
145                 150                 155                 160

Leu His Gly Leu Ile His Asn Val Leu Pro Tyr Val Gly Thr Ser Val
                165                 170                 175

Lys Thr Leu Val Leu Ala Tyr Ser Ser Ala Val Ser Ser Lys Met Val
            180                 185                 190

Arg Gln Ile Leu Glu Leu Cys Pro Asn Leu Glu His Leu Asp Leu Thr
```

```
          195                 200                 205

Gln Thr Asp Ile Ser Asp Ser Ala Phe Asp Ser Trp Ser Trp Leu Gly
      210                 215                 220

Cys Cys Gln Ser Leu Arg His Leu Asp Leu Ser Gly Cys Glu Lys Ile
225                 230                 235                 240

Thr Asp Val Ala Leu Glu Lys Ile Ser Arg Ala Leu Gly Ile Leu Thr
                245                 250                 255

Ser His Gln Ser Gly Phe Leu Lys Thr Ser Thr Ser Lys Ile Thr Ser
            260                 265                 270

Thr Ala Trp Lys Asn Lys Asp Ile Thr Met Gln Ser Thr Lys Gln Tyr
        275                 280                 285

Ala Cys Leu His Asp Leu Thr Asn Lys Gly Ile Gly Glu Glu Ile Asp
    290                 295                 300

Asn Glu His Pro Trp Thr Lys Pro Val Ser Ser Glu Asn Phe Thr Ser
305                 310                 315                 320

Pro Tyr Val Trp Met Leu Asp Ala Glu Asp Leu Ala Asp Ile Glu Asp
                325                 330                 335

Thr Val Glu Trp Arg His Arg Asn Val Glu Ser Leu Cys Val Met Glu
            340                 345                 350

Thr Ala Ser Asn Phe Ser Cys Ser Thr Ser Gly Cys Phe Ser Lys Asp
        355                 360                 365

Ile Val Gly Leu Arg Thr Ser Val Cys Trp Gln Gln His Cys Ala Ser
    370                 375                 380

Pro Ala Phe Ala Tyr Cys Gly His Ser Phe Cys Cys Thr Gly Thr Ala
385                 390                 395                 400

Leu Arg Thr Met Ser Ser Leu Pro Glu Ser Ser Ala Met Cys Arg Lys
                405                 410                 415

Ala Ala Arg Thr Arg Leu Pro Arg Gly Lys Asp Leu Ile Tyr Phe Gly
            420                 425                 430

Ser Glu Lys Ser Asp Gln Glu Thr Gly Arg Val Leu Leu Phe Leu Ser
        435                 440                 445

Leu Ser Gly Cys Tyr Gln Ile Thr Asp His Gly Leu Arg Val Leu Thr
    450                 455                 460

Leu Gly Gly Gly Leu Pro Tyr Leu Glu His Leu Asn Leu Ser Gly Cys
465                 470                 475                 480

Leu Thr Ile Thr Gly Ala Gly Leu Gln Asp Leu Val Ser Ala Cys Pro
                485                 490                 495

Ser Leu Asn Asp Glu Tyr Phe Tyr Tyr Cys Asp Asn Ile Asn Gly Pro
            500                 505                 510

His Ala Asp Thr Ala Ser Gly Cys Gln Asn Leu Gln Cys Gly Phe Arg
        515                 520                 525

Ala Cys Cys Arg Ser Gly Glu Pro Leu Thr Ser Asp Leu Cys Leu Leu
```

```
    530                 535                 540

His Leu Ala Glu Gln Ala Phe Phe His Ala Leu Tyr Ser His Ile Ser
545                 550                 555                 560

Cys Val Asn His Pro Phe Leu Ser Val Thr Cys Phe Gly Pro Ile Xaa
                565                 570                 575

Tyr Asn Phe Arg Asn Leu Asn Tyr Gln Xaa Ile Val Met Leu
            580                 585                 590
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<210> 53
<211> 1681
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> all n positions
<223> n=a, c, g or t

<400> 53
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gagggcaaaa ggagcactag ctaggtcaga gccatgtttc aggtcacaat gtgatgtcag 180
atgttgctta taaatccttt cttgtcttcg ccattcttaa atcttgatag gtgcctgttg 240
ggaaactgta aatgcctttc ccaatggaga atcaacagat tgggtgatgg tggagtcggt 300
caggaagact caggtcttct agaggaaagg atgcctcatc acccccttngg cccaggcagc 360
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ggtggggtga cgggagcaaa gtaggcgtgg actttgacat gagggagctg agcccgcatc 480
cgcttgatgc ctgcacgggt aacctgctgg cagtcgtaca gctcgaggcg ctccaggcct 540
cggcagttct ctaggtgtyc cagggccaca tcagtgatga ggaggcagtt gtccaactcc 600
agtacccgca gcctctcatg gccacaggta ctgttgctca ggtgcaggat cccatcatct 660
gkgatgagtt cacagtggga caggctcagg gcttgcagtt taggacagtg aatggagagc 720
tggatgagtg tgctgtcggt tatcaggatg cawtcttcaa gatccatctt ctccaattcg 780
tggcaattcc gagctaaaag tgtaaaacct gcgtcagtca aatgggagca tcgggcagcc 840
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ttgctgcaac ccgaaaggca gagagcctgt agccggtgac agcccctgca tatctgcacc 960
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gctttcaggc ctcgacaacc tcgcaccagt gcctcgatgc catccttcgt gatctgatca 1140
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ctgtttgtaa tagacacaca ggaggtcaga wccagatgtt tcagcttgga acagaatctg 1260
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ccctctacat ctatttgaaa gttaaaaaga tctattcttt gccagttgct tccatccagg 1500
gctaagatgt tccaagcctt ggaaatctgt gcacatcggc acaaagttac tatatccaag 1560
aaggaaaata ttcttaacag aagttctttg ggtaactttt tgttaataag gccttcatca 1620
ttgtttgaga aaaccatggc cgaagagccg cgagcgagcc cacagcccga agtcacacgg 1680
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<210> 54
<211> 437
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> all Xaa positions
<223> Xaa=unknown amino acid residue

<400> 54

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Phe Ser Asn Asn Asp Glu Gly Leu Ile Asn Lys Lys Leu Pro Lys Glu
            20                  25                  30

Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val Thr Leu Cys Arg
        35                  40                  45

Cys Ala Gln Ile Ser Lys Ala Trp Asn Ile Leu Ala Leu Asp Gly Ser
    50                  55                  60

Asn Trp Gln Arg Ile Asp Leu Phe Asn Phe Gln Ile Asp Val Glu Gly
65                  70                  75                  80

Arg Val Val Glu Asn Ile Ser Lys Arg Cys Val Gly Phe Leu Arg Lys
                85                  90                  95

Leu Ser Leu Arg Gly Cys Ile Gly Val Gly Asp Ser Ser Leu Lys Thr
            100                 105                 110

Phe Ala Gln Asn Cys Arg Asn Ile Glu His Leu Asn Leu Asn Gly Cys
        115                 120                 125

Thr Lys Ile Thr Asp Ser Thr Cys Tyr Ser Leu Ser Arg Phe Cys Ser
    130                 135                 140

Lys Leu Lys His Leu Xaa Leu Thr Ser Cys Val Ser Ile Thr Asn Ser
145                 150                 155                 160

Ser Leu Lys Gly Ile Ser Glu Gly Cys Arg Asn Leu Glu Tyr Leu Asn
                165                 170                 175

Leu Ser Trp Cys Asp Gln Ile Thr Lys Asp Gly Ile Glu Ala Leu Val
            180                 185                 190

Arg Gly Cys Arg Gly Leu Lys Ala Leu Leu Leu Arg Gly Cys Thr Gln
        195                 200                 205

Leu Glu Asp Glu Ala Leu Lys His Ile Gln Asn Tyr Cys His Glu Leu
    210                 215                 220

Val Ser Leu Asn Leu Gln Ser Cys Ser Arg Ile Thr Asp Glu Gly Val
225                 230                 235                 240

Val Gln Ile Cys Arg Gly Cys His Arg Leu Gln Ala Leu Cys Leu Ser
                245                 250                 255

Gly Cys Ser Asn Leu Thr Asp Ala Ser Leu Thr Ala Leu Gly Leu Asn
            260                 265                 270

Cys Pro Arg Leu Gln Ile Leu Glu Ala Ala Arg Cys Ser His Leu Thr
        275                 280                 285

Asp Ala Gly Phe Thr Leu Leu Ala Arg Asn Cys His Glu Leu Glu Lys
    290                 295                 300

Met Asp Leu Glu Xaa Cys Ile Leu Ile Thr Asp Ser Thr Leu Ile Gln
305                 310                 315                 320

Leu Ser Ile His Cys Pro Lys Leu Gln Ala Leu Ser Leu Ser His Cys
                325                 330                 335
```

Glu Leu Ile Xaa Asp Asp Gly Ile Leu His Leu Ser Asn Ser Thr Cys
340 345 350

Gly His Glu Arg Leu Arg Val Leu Glu Leu Asp Asn Cys Leu Leu Ile
355 360 365

Thr Asp Val Ala Leu Xaa His Leu Glu Asn Cys Arg Gly Leu Glu Arg
370 375 380

Leu Glu Leu Tyr Asp Cys Gln Gln Val Thr Arg Ala Gly Ile Lys Arg
385 390 395 400

Met Arg Ala Gln Leu Pro His Val Lys Val His Ala Tyr Phe Ala Pro
405 410 415

Val Thr Pro Pro Thr Ala Val Ala Gly Ser Gly Gln Arg Leu Cys Arg
420 425 430

Cys Cys Val Ile Leu
435

<210> 55
<211> 1866
<212> DNA
<213> Homo sapiens

<400> 55
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cgccgagcca ggacagctac aagaggagaa atgatgaaca cccatagagc tatagaatca 120
aacagccaga cttcccctct caatgcagag gtagtccagt atgccaaaga agtagtggat 180
ttcagttccc attatggaag tgagaatagt atgtcctata ctatgtggaa tttggctggt 240
gtaccaaatg tattcccaag ttctggtgac tttactcaga cagctgtgtt tcgaacttat 300
gggacatggt gggatcagtg tcctagtgct tccttgccat tcaagaggac gccacctaat 360
tttcagagcc aggactatgt ggaacttact tttgaacaac aggtgtatcc tacagctgta 420
catgttctag aaacctatca tcccggagca gtcattagaa ttctcgcttg ttctgcaaat 480
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acgaaggtga atgcttccca agctcgccag tttaaacctt gtattaagca gataaatttc 600
cccacaaatc ttatacgact ggaagtaaat agttctcttc tggaatatta cactgaatta 660
gatgcagttg tgctacatgg tgtgaaggac aagccagtgc tttctctcaa gacttcactt 720
attgacatga atgatataga agatgatgcc tatgcagaaa aggatggttg tggaatggac 780
agtcttaaca aaaagtttag cagtgctgtc ctcggggaag ggccaaataa tgggtatttt 840
gataaactac cttatgagct tattcagctg attctgaatc atcttacact accagacctg 900
tgtagattag cacagacttg caaactactg agccagcatt gctgtgatcc tctgcaatac 960
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gaattgtctt gcagccactt tcttaatgaa acttgcttag aagttatttc tgagatgtgt 1200
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agcaccgggt gcttcaccag actggcacac cagctcccaa acttgcaaaa actctttctt 1620
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ctggaatctt gtaaagatct ttctttactt gatgtgtcct tctgttcgca gattgataac 1800
agagctgtgc tagaactgaa tgcaagcttt ccaaaagtgt tcataaaaaa gagctttact 1860
cagtga 1866

<210> 56
<211> 621

<212> PRT
<213> Homo sapiens

<400> 56

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Met Ser Pro Val Phe Pro Met Leu Thr Val Leu Thr Met Phe Tyr Tyr
 1               5                  10                  15

Ile Cys Leu Arg Arg Arg Ala Arg Thr Ala Thr Arg Gly Glu Met Met
            20                  25                  30

Asn Thr His Arg Ala Ile Glu Ser Asn Ser Gln Thr Ser Pro Leu Asn
        35                  40                  45

Ala Glu Val Val Gln Tyr Ala Lys Glu Val Val Asp Phe Ser Ser His
    50                  55                  60

Tyr Gly Ser Glu Asn Ser Met Ser Tyr Thr Met Trp Asn Leu Ala Gly
65                  70                  75                  80

Val Pro Asn Val Phe Pro Ser Ser Gly Asp Phe Thr Gln Thr Ala Val
                85                  90                  95

Phe Arg Thr Tyr Gly Thr Trp Trp Asp Gln Cys Pro Ser Ala Ser Leu
            100                 105                 110

Pro Phe Lys Arg Thr Pro Pro Asn Phe Gln Ser Gln Asp Tyr Val Glu
        115                 120                 125

Leu Thr Phe Glu Gln Gln Val Tyr Pro Thr Ala Val His Val Leu Glu
    130                 135                 140

Thr Tyr His Pro Gly Ala Val Ile Arg Ile Leu Ala Cys Ser Ala Asn
145                 150                 155                 160

Pro Tyr Ser Pro Asn Pro Pro Ala Glu Val Arg Trp Glu Ile Leu Trp
                165                 170                 175

Ser Glu Arg Pro Thr Lys Val Asn Ala Ser Gln Ala Arg Gln Phe Lys
            180                 185                 190

Pro Cys Ile Lys Gln Ile Asn Phe Pro Thr Asn Leu Ile Arg Leu Glu
        195                 200                 205

Val Asn Ser Ser Leu Leu Glu Tyr Tyr Thr Glu Leu Asp Ala Val Val
    210                 215                 220

Leu His Gly Val Lys Asp Lys Pro Val Leu Ser Leu Lys Thr Ser Leu
225                 230                 235                 240

Ile Asp Met Asn Asp Ile Glu Asp Asp Ala Tyr Ala Glu Lys Asp Gly
                245                 250                 255

Cys Gly Met Asp Ser Leu Asn Lys Lys Phe Ser Ser Ala Val Leu Gly
            260                 265                 270

Glu Gly Pro Asn Asn Gly Tyr Phe Asp Lys Leu Pro Tyr Glu Leu Ile
        275                 280                 285

Gln Leu Ile Leu Asn His Leu Thr Leu Pro Asp Leu Cys Arg Leu Ala
    290                 295                 300

Gln Thr Cys Lys Leu Leu Ser Gln His Cys Cys Asp Pro Leu Gln Tyr
305                 310                 315                 320
```

Ile His Leu Asn Leu Gln Pro Tyr Trp Ala Lys Leu Asp Asp Thr Ser
325 330 335

Leu Glu Phe Leu Gln Ser Arg Cys Thr Leu Val Gln Trp Leu Asn Leu
340 345 350

Ser Trp Thr Gly Asn Arg Gly Phe Ile Ser Val Ala Gly Phe Ser Arg
355 360 365

Phe Leu Lys Val Cys Gly Ser Glu Leu Val Arg Leu Glu Leu Ser Cys
370 375 380

Ser His Phe Leu Asn Glu Thr Cys Leu Glu Val Ile Ser Glu Met Cys
385 390 395 400

Pro Asn Leu Gln Ala Leu Asn Leu Ser Ser Cys Asp Lys Leu Pro Pro
405 410 415

Gln Ala Phe Asn His Ile Ala Lys Leu Cys Ser Leu Lys Arg Leu Val
420 425 430

Leu Tyr Arg Thr Lys Val Glu Gln Thr Ala Leu Leu Ser Ile Leu Asn
435 440 445

Phe Cys Ser Glu Leu Gln His Leu Ser Leu Gly Ser Cys Val Met Ile
450 455 460

Glu Asp Tyr Asp Val Ile Ala Ser Met Ile Gly Ala Lys Cys Lys Lys
465 470 475 480

Leu Arg Thr Leu Asp Leu Trp Arg Cys Lys Asn Ile Thr Glu Asn Gly
485 490 495

Ile Ala Glu Leu Ala Ser Gly Cys Pro Leu Leu Glu Glu Leu Asp Leu
500 505 510

Gly Trp Cys Pro Thr Leu Gln Ser Ser Thr Gly Cys Phe Thr Arg Leu
515 520 525

Ala His Gln Leu Pro Asn Leu Gln Lys Leu Phe Leu Thr Ala Asn Arg
530 535 540

Ser Val Cys Asp Thr Asp Ile Asp Glu Leu Ala Cys Asn Cys Thr Arg
545 550 555 560

Leu Gln Gln Leu Asp Ile Leu Gly Thr Arg Met Val Ser Pro Ala Ser
565 570 575

Leu Arg Lys Leu Leu Glu Ser Cys Lys Asp Leu Ser Leu Leu Asp Val
580 585 590

Ser Phe Cys Ser Gln Ile Asp Asn Arg Ala Val Leu Glu Leu Asn Ala
595 600 605

Ser Phe Pro Lys Val Phe Ile Lys Lys Ser Phe Thr Gln
610 615 620

<210> 57
<211> 984
<212> DNA
<213> Homo sapiens

<400> 57
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ggcgttggaa acagctacat tgaagataat gatgatgaca gcaaaatggc agatctcttg 120
tcctacttcc agcagcaact cacatttcag gagtctgtgc ttaaactgtg tcagcctgag 180
cttgagagca gtcagattca catatcagtg ctgccaatgg aggtcctgat gtacatcttc 240
cgatgggtgg tgtctagtga cttggacctc agatcattgg agcagttgtc gctggtgtgc 300
agaggattct acatctgtgc cagagaccct gaaatatggc gtctggcctg cttgaaagtt 360
tggggcagaa gctgtattaa acttgttccg tacacgtcct ggagagagat gtttttagaa 420
cggcctcgtg ttcggtttga tggcgtgtat atcagtaaaa ccacatatat tcgtcaaggg 480
gaacagtctc ttgatggttt ctatagagcc tggcaccaag tggaatatta caggtacata 540
agattctttc ctgatggcca tgtgatgatg ttgacaaccc ctgaagagcc tcagtccatt 600
gttccacgtt taagaactag gaataccagg actgatgcaa ttctactggg tcactatcgc 660
ttgtcacaag acacagacaa tcagaccaaa gtatttgctg taataactaa gaaaaaagaa 720
gaaaaaccac ttgactataa atacagatat tttcgtcgtg tccctgtaca agaagcagat 780
cagagttttc atgtggggct acagctatgt tccagtggtc accagaggtt caacaaactc 840
atctggatac atcattcttg tcacattact tacaaatcaa ctggtgagac tgcagtcagt 900
gcttttgaga ttgacaagat gtacaccccc ttgttcttcg ccagagtaag gagctacaca 960
gctttctcag aaaggcctct gtag 984

<210> 58
<211> 327
<212> PRT
<213> Homo sapiens

<400> 58
Met Gln Leu Val Pro Asp Ile Glu Phe Lys Ile Thr Tyr Thr Arg Ser
1 5 10 15

Pro Asp Gly Asp Gly Val Gly Asn Ser Tyr Ile Glu Asp Asn Asp Asp
20 25 30

Asp Ser Lys Met Ala Asp Leu Leu Ser Tyr Phe Gln Gln Gln Leu Thr
35 40 45

Phe Gln Glu Ser Val Leu Lys Leu Cys Gln Pro Glu Leu Glu Ser Ser
50 55 60

Gln Ile His Ile Ser Val Leu Pro Met Glu Val Leu Met Tyr Ile Phe
65 70 75 80

Arg Trp Val Val Ser Ser Asp Leu Asp Leu Arg Ser Leu Glu Gln Leu
85 90 95

Ser Leu Val Cys Arg Gly Phe Tyr Ile Cys Ala Arg Asp Pro Glu Ile
100 105 110

Trp Arg Leu Ala Cys Leu Lys Val Trp Gly Arg Ser Cys Ile Lys Leu
115 120 125

Val Pro Tyr Thr Ser Trp Arg Glu Met Phe Leu Glu Arg Pro Arg Val
130 135 140

Arg Phe Asp Gly Val Tyr Ile Ser Lys Thr Thr Tyr Ile Arg Gln Gly
145 150 155 160

Glu Gln Ser Leu Asp Gly Phe Tyr Arg Ala Trp His Gln Val Glu Tyr
165 170 175

Tyr Arg Tyr Ile Arg Phe Phe Pro Asp Gly His Val Met Met Leu Thr
180 185 190

Thr Pro Glu Glu Pro Gln Ser Ile Val Pro Arg Leu Arg Thr Arg Asn
195 200 205

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Thr Arg Thr Asp Ala Ile Leu Leu Gly His Tyr Arg Leu Ser Gln Asp
    210                 215                 220

Thr Asp Asn Gln Thr Lys Val Phe Ala Val Ile Thr Lys Lys Lys Glu
225                 230                 235                 240

Glu Lys Pro Leu Asp Tyr Lys Tyr Arg Tyr Phe Arg Arg Val Pro Val
                245                 250                 255

Gln Glu Ala Asp Gln Ser Phe His Val Gly Leu Gln Leu Cys Ser Ser
            260                 265                 270

Gly His Gln Arg Phe Asn Lys Leu Ile Trp Ile His His Ser Cys His
        275                 280                 285

Ile Thr Tyr Lys Ser Thr Gly Glu Thr Ala Val Ser Ala Phe Glu Ile
    290                 295                 300

Asp Lys Met Tyr Thr Pro Leu Phe Phe Ala Arg Val Arg Ser Tyr Thr
305                 310                 315                 320

Ala Phe Ser Glu Arg Pro Leu
                325
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<210> 59
<211> 765
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> all n positions
<223> n=a, c, g or t

<400> 59
gcagccctgg atcctgactt agagaatgat gatttctttg tcagaaagac tggggctttc 60
catgcaaatc catatgttct ccgagctttt gaagacttta gaaagttctc tgagcaagat 120
gattctgtag agcgagatat aattttacag tgtagaggaag gtgaacttgt acttccggat 180
ttggaaaaag atgatatgat tgttcgccga atcccagcac agaagaaaga agtgccgctg 240
tctggggccc cagatagata ccacccagtc ccttttcccg aaccctggac tcttcctcca 300
gaaattcaag caaaatttct ctgtgtactt gaaaggacat gcccatccaa agaaaaaagt 360
aatagctgta gaatattagt tccttcatat cggcagaaga aagatgacat gctgacacgt 420
aagattcagt cctggaaact gggaactacc gtgcctccca tcagtttcac ncctggcccc 480
tgcagtgagg ctgacttgaa gagatgggag gccatccggg aggccagcag actcaggcac 540
aagaaaaggc tgatggtgga gagactcttt caaaagattt atggtgagaa tgggagtaag 600
tccatgagtg atgtcagcgc agaagatgtt caaaacttgc gtcagctgcg ttacgaggag 660
atgcagaaaa taaaatcaca attaaaagaa caagatcaga aatggcagga tgaccttgca 720
aaatggaaag atcgtcgaaa aagttacact tcagatctgc agaag 765

<210> 60
<211> 255
<212> PRT
<213> Homo sapiens

<400> 60
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Ala Ala Leu Asp Pro Asp Leu Glu Asn Asp Asp Phe Phe Val Arg Lys
  1               5                  10                  15

Thr Gly Ala Phe His Ala Asn Pro Tyr Val Leu Arg Ala Phe Glu Asp
            20                  25                  30

Phe Arg Lys Phe Ser Glu Gln Asp Asp Ser Val Glu Arg Asp Ile Ile
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         35                  40                  45

Leu Gln Cys Arg Glu Gly Glu Leu Val Leu Pro Asp Leu Glu Lys Asp
     50                  55                  60

Asp Met Ile Val Arg Arg Ile Pro Ala Gln Lys Lys Glu Val Pro Leu
 65                  70                  75                  80

Ser Gly Ala Pro Asp Arg Tyr His Pro Val Pro Phe Pro Glu Pro Trp
                 85                  90                  95

Thr Leu Pro Pro Glu Ile Gln Ala Lys Phe Leu Cys Val Leu Glu Arg
            100                 105                 110

Thr Cys Pro Ser Lys Glu Lys Ser Asn Ser Cys Arg Ile Leu Val Pro
        115                 120                 125

Ser Tyr Arg Gln Lys Lys Asp Asp Met Leu Thr Arg Lys Ile Gln Ser
    130                 135                 140

Trp Lys Leu Gly Thr Thr Val Pro Pro Ile Ser Phe Thr Pro Gly Pro
145                 150                 155                 160

Cys Ser Glu Ala Asp Leu Lys Arg Trp Glu Ala Ile Arg Glu Ala Ser
                165                 170                 175

Arg Leu Arg His Lys Lys Arg Leu Met Val Glu Arg Leu Phe Gln Lys
            180                 185                 190

Ile Tyr Gly Glu Asn Gly Ser Lys Ser Met Ser Asp Val Ser Ala Glu
        195                 200                 205

Asp Val Gln Asn Leu Arg Gln Leu Arg Tyr Glu Glu Met Gln Lys Ile
    210                 215                 220

Lys Ser Gln Leu Lys Glu Gln Asp Gln Lys Trp Gln Asp Asp Leu Ala
225                 230                 235                 240

Lys Trp Lys Asp Arg Arg Lys Ser Tyr Thr Ser Asp Leu Gln Lys
                245                 250                 255


<210> 61
<211> 36
<212> PRT
<213> Homo sapiens

<400> 61
Leu Pro Pro Glu Leu Ser Phe Thr Ile Leu Ser Tyr Leu Asn Ala Thr
  1                 5                  10                  15

Asp Leu Cys Leu Ala Ser Cys Val Trp Gln Asp Leu Ala Asn Asp Glu
             20                  25                  30

Leu Leu Trp Gln
         35


<210> 62
<211> 42
<212> PRT
<213> Homo sapiens
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<400> 62
Leu Pro Gly Glu Val Leu Glu Tyr Ile Leu Cys Cys Gly Ser Leu Thr
1 5 10 15

Ala Ala Asp Ile Gly Arg Val Ser Ser Thr Cys Arg Arg Leu Arg Glu
20 25 30

Leu Cys Gln Ser Ser Gly Lys Val Trp Lys
35 40

<210> 63
<211> 44
<212> PRT
<213> Homo sapiens

<400> 63
Leu Ala Glu Val Val Glu Arg Val Leu Thr Phe Leu Pro Ala Lys Ala
1 5 10 15

Leu Leu Arg Val Ala Cys Val Cys Arg Leu Trp Arg Glu Cys Val Arg
20 25 30

Arg Val Leu Arg Thr His Arg Ser Val Thr Trp Ile
35 40

<210> 64
<211> 39
<212> PRT
<213> Homo sapiens

<400> 64
Leu Pro Asp Glu Val Val Leu Lys Ile Phe Ser Tyr Leu Leu Glu Gln
1 5 10 15

Asp Leu Cys Arg Ala Ala Cys Val Cys Lys Arg Phe Ser Glu Leu Ala
20 25 30

Asn Asp Pro Asn Leu Trp Lys
35

<210> 65
<211> 41
<212> PRT
<213> Homo sapiens

<400> 65
Leu Pro Leu Glu Leu Trp Arg Met Ile Leu Ala Tyr Leu His Leu Pro
1 5 10 15

Asp Leu Gly Arg Cys Ser Leu Val Cys Arg Ala Trp Tyr Glu Leu Ile
20 25 30

Leu Ser Leu Asp Ser Thr Arg Trp Arg
35 40

<210> 66
<211> 39
<212> PRT
<213> Homo sapiens

<400> 66
Leu Pro Thr Asp Pro Leu Leu Leu Ile Leu Ser Phe Leu Asp Tyr Arg
1 5 10 15

Asp Leu Ile Asn Cys Cys Tyr Val Ser Arg Arg Leu Ser Gln Leu Ser
20 25 30

Ser His Asp Pro Leu Trp Arg
35

<210> 67
<211> 40
<212> PRT
<213> Homo sapiens

<400> 67
Leu Pro Glu Pro Leu Leu Leu Arg Val Leu Ala Ala Leu Pro Ala Ala
1 5 10 15

Glu Leu Val Gln Ala Cys Arg Leu Val Cys Leu Arg Trp Lys Glu Leu
20 25 30

Val Asp Gly Ala Pro Leu Trp Leu
35 40

<210> 68
<211> 40
<212> PRT
<213> Homo sapiens

<400> 68
Leu Phe Pro Pro Glu Leu Val Glu His Ile Ile Ser Phe Leu Pro Val
1 5 10 15

Arg Asp Leu Val Ala Leu Gly Gln Thr Cys Arg Tyr Phe His Glu Val
20 25 30

Cys Asp Gly Glu Gly Val Trp Arg
35 40

<210> 69
<211> 44
<212> PRT
<213> Homo sapiens

<400> 69
Leu Pro Glu Val Leu Leu Leu His Met Cys Ser Tyr Leu Asp Met Arg
1 5 10 15

Ala Leu Gly Arg Leu Ala Gln Val Tyr Arg Trp Leu Trp His Phe Thr
20 25 30

Asn Cys Asp Leu Leu Arg Arg Gln Ile Ala Trp Ala
35 40

<210> 70
<211> 40
<212> PRT
<213> Homo sapiens

<400> 70
Leu Pro Leu His Met Leu Asn Asn Ile Leu Tyr Arg Phe Ser Asp Gly
1 5 10 15

Trp Asp Ile Ile Thr Leu Gly Gln Val Thr Pro Thr Leu Tyr Met Leu
20 25 30

Ser Glu Asp Arg Gln Leu Trp Lys
35 40

<210> 71
<211> 39
<212> PRT
<213> Homo sapiens

<400> 71
Leu Pro Asp His Ser Met Val Gln Ile Phe Ser Phe Leu Pro Thr Asn
1 5 10 15

Gln Leu Cys Arg Cys Ala Arg Val Cys Arg Arg Trp Tyr Asn Leu Ala
20 25 30

Trp Asp Pro Arg Leu Trp Arg
35

<210> 72
<211> 44
<212> PRT
<213> Homo sapiens

<400> 72
Ile Pro Leu Glu Ile Leu Val Gln Ile Phe Gly Leu Leu Val Ala Ala
1 5 10 15

Asp Gly Pro Met Pro Phe Leu Gly Arg Ala Ala Arg Val Cys Arg Arg
20 25 30

Trp Gln Glu Ala Ala Ser Gln Pro Ala Leu Trp His
35 40

<210> 73
<211> 39
<212> PRT
<213> Homo sapiens

<400> 73
Leu Pro Pro Glu Val Met Leu Ser Ile Phe Ser Tyr Leu Asn Pro Gln
1 5 10 15

Glu Leu Cys Arg Cys Ser Gln Val Ser Met Lys Trp Ser Gln Leu Thr
20 25 30

Lys Thr Gly Ser Leu Trp Lys
35

<210> 74
<211> 39
<212> PRT
<213> Homo sapiens

<400> 74
Leu Pro Lys Glu Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val
1 5 10 15

Thr Leu Cys Arg Cys Ala Gln Ile Ser Lys Ala Trp Asn Ile Leu Ala
20 25 30

Leu Asp Gly Ser Asn Trp Gln
35

<210> 75
<211> 48
<212> PRT
<213> Homo sapiens

<400> 75
Leu Pro Tyr Glu Leu Ile Gln Leu Ile Leu Asn His Leu Thr Leu Pro
1 5 10 15

Asp Leu Cys Arg Leu Ala Gln Thr Cys Lys Leu Leu Ser Gln His Cys
20 25 30

Cys Asp Pro Leu Gln Tyr Ile His Leu Asn Leu Gln Pro Tyr Trp Ala
35 40 45

<210> 76
<211> 44
<212> PRT
<213> Homo sapiens

<400> 76
Leu Pro Met Glu Val Leu Met Tyr Ile Phe Arg Trp Val Val Ser Ser
1 5 10 15

Asp Leu Asp Leu Arg Ser Leu Glu Gln Leu Ser Leu Val Cys Arg Gly
20 25 30

Phe Tyr Ile Cys Ala Arg Asp Pro Glu Ile Trp Arg
35 40

<210> 77
<211> 49
<212> PRT
<213> Homo sapiens

<400> 77
Leu Pro Pro Glu Ile Gln Ala Lys Phe Leu Cys Val Leu Glu Arg Thr
1 5 10 15

Cys Pro Ser Lys Glu Lys Ser Asn Ser Cys Arg Ile Leu Val Pro Ser
20 25 30

Tyr Arg Gln Lys Lys Asp Asp Met Leu Thr Arg Lys Ile Gln Ser Trp
35 40 45

Lys

<210> 78
<211> 39
<212> PRT
<213> Homo sapiens

<400> 78
Leu Pro His His Val Val Leu Gln Ile Phe Gln Tyr Leu Pro Leu Leu
1 5 10 15

Asp Arg Ala Cys Ala Ser Ser Val Cys Arg Arg Trp Asn Glu Val Phe
20 25 30

His Ile Ser Asp Leu Trp Arg
35

<210> 79
<211> 43
<212> PRT
<213> Homo sapiens

<400> 79
Leu Trp Ala Trp Gly Glu Lys Gly Val Leu Ser Asn Ile Ser Ala Leu
1 5 10 15

Thr Asp Leu Gly Gly Leu Asp Pro Val Trp Leu Val Cys Gly Ser Trp
20 25 30

Arg Arg His Val Gly Ala Gly Leu Cys Trp Ala
35 40

<210> 80
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 80
agtagtaaca aaggtcaaag acagttgact gtatcgtcga ggatgccttc aattaagtt 59

<210> 81
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 81
gcggttactt acttagagct cgacgtctta cttacttagc tcacttctct tcacacca 58

<210> 82
<211> 12
<212> PRT
<213> Homo sapiens

<400> 82

Cys Asp Gly Glu Lys Asp Thr Tyr Ser Tyr Leu Ala
1 5 10

<210> 83
<211> 25
<212> PRT
<213> Homo sapiens

<400> 83
Cys Glu Ser Ser Phe Ser Leu Asn Met Asn Phe Ser Ser Lys Arg Thr
1 5 10 15

Lys Phe Lys Ile Thr Thr Ser Met Gln
20 25

<210> 84
<211> 12
<212> PRT
<213> Homo sapiens

<400> 84
Cys Glu Glu Ala Gln Val Arg Lys Glu Asn Gln Trp
1 5 10

<210> 85
<211> 19
<212> PRT
<213> Homo sapiens

<400> 85
Asn Ala Gly Ser Val Glu Gln Thr Pro Lys Lys Pro Gly Leu Arg Arg
1 5 10 15

Arg Gln Thr

<210> 86
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 86
cctgggggat gttctca 17

<210> 87
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 87
ggcttccggg catttag 17

<210> 88
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 88
catctggcac gattcca 17

<210> 89
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 89
ccgctcatcg tatgaca 17